		(glio/astro) U87-MG	
Lung	0.1	CNS cancer (glio/astro) U-118-MG	3.2
Fetal Lung	1.6	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	20.2
Lung ca. LX-1	3.6	CNS cancer (astro) SNB-75	33.4
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.1
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	12.2
Lung ca. A549	8.8	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	0.1
Lung ca. NCI-H460	12.6	Brain (Hippocampus) Pool	0.1
Lung ca. HOP-62	4.3	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.7	Brain (Thalamus) Pool	0.0
Fetal Liver	2.2	Brain (whole)	0.1
Liver ca. HepG2	2.4	Spinal Cord Pool	0.1
Kidney Pool	0.3	Adrenal Gland	0.3
Fetal Kidney	0.6	Pituitary gland Pool	0.1
Renal ca. 786-0	18.6	Salivary Gland	0.1
Renal ca. A498	6.5	Thyroid (female)	0.1
Renal ca. ACHN	1.6	Pancreatic ca. CAPAN2	3.7
Renal ca. UO-31	1.3	Pancreas Pool	0.5

Table LC. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag2049, Run 165626390	Rel. Exp.(%) Ag2049, Run 165627405	Tissue Name	Rel. Exp.(%) Ag2049, Run 165626390	Rel. Exp.(%) Ag2049, Run 165627405
Liver adenocarcinoma	0.0	0.0	Kidney (fetal)	1.6	1.3
Pancreas	0.1	0.1	Renal ca. 786-0	49.0	44.8
Pancreatic ca. CAPAN 2	10.1	10.5	Renal ca. A498	49.3	47.3
Adrenal gland	0.6	0.5	Renal ca. RXF 393	35.4	30.6
Thyroid	0.2	0.3	Renal ca. ACHN	2.9	2.7
Salivary gland	0.1	0.2	Renal ca. UO-31	9.9	11.7
Pituitary gland	0.2	0.1	Renal ca. TK-10	2.2	2.3
Brain (fetal)	0.2	0.2	Liver	0.8	0.8
Brain (whole)	0.2	0.2	Liver (fetal)	4.3	4.7
Brain (amygdala)	0.2	0.2	Liver ca. (hepatoblast) HepG2	9.9	8.7
Brain (cerebellum)	0.1	0.1	Lung	1.4	1.0
Brain (hippocampus)	0.2	0.3	Lung (fetal)	3.0	2.7
Brain (substantia nigra)	0.1	0.1	Lung ca. (small cell) LX-1	8.0	8.8
Brain (thalamus)	0.2	0.4	Lung ca. (small cell) NCI-H69	0.2	0.1
Cerebral Cortex	0.1	0.1	Lung ca. (s.cell var.) SHP-77	0.0	0.0
Spinal cord	0.9	0.7	Lung ca. (large cell)NCI-H460	50.7	40.1
glio/astro U87-MG	10.7	12.0	Lung ca. (non-sm. cell) A549	3.5	3.1

glio/astro U-118-MG	10.9	18.0	Lung ca. (non-s.cell) NCI-H23	0.1	0.1
astrocytoma SW1783	93.3	**100.0**	Lung ca. (non-s.cell) HOP-62	14.4	13.3
neuro*; met SK-N-AS	0.1	0.1	Lung ca. (non-s.cl) NCI-H522	0.0	0.0
astrocytoma SF-539	14.1	13.9	Lung ca. (squam.) SW 900	3.5	2.7
astrocytoma SNB-75	**100.0**	93.3	Lung ca. (squam.) NCI-H596	0.0	0.0
glioma SNB-19	2.2	1.9	Mammary gland	1.5	1.1
glioma U251	78.5	64.6	Breast ca.* (pl.ef) MCF-7	0.1	0.1
glioma SF-295	20.4	25.2	Breast ca.* (pl.ef) MDA-MB-231	7.7	6.8
Heart (fetal)	0.6	0.8	Breast ca.* (pl.ef) T47D	0.0	0.0
Heart	1.0	0.8	Breast ca. BT-549	7.2	6.8
Skeletal muscle (fetal)	1.9	1.7	Breast ca. MDA-N	0.7	0.8
Skeletal muscle	0.6	0.9	Ovary	0.6	0.7
Bone marrow	0.3	0.4	Ovarian ca. OVCAR-3	0.0	0.0
Thymus	0.4	0.4	Ovarian ca. OVCAR-4	0.3	0.4
Spleen	2.1	1.8	Ovarian ca. OVCAR-5	10.5	10.4
Lymph node	3.1	2.5	Ovarian ca. OVCAR-8	2.7	2.9
Colorectal	1.4	1.0	Ovarian ca. IGROV-1	0.0	0.0
Stomach	0.9	0.8	Ovarian ca.* (ascites) SK-OV-3	9.8	11.8
Small intestine	3.1	3.3	Uterus	2.1	2.0
Colon ca. SW480	1.2	1.4	Placenta	0.6	1.4

Colon ca.* SW620(SW480 met)	1.5	1.7	Prostate	0.2	0.2
Colon ca. HT29	0.1	0.2	Prostate ca.* (bone met)PC-3	0.0	0.0
Colon ca. HCT-116	0.0	0.0	Testis	0.1	0.1
Colon ca. CaCo-2	1.1	1.4	Melanoma Hs688(A).T	26.2	23.8
Colon ca. tissue(ODO3866)	10.2	9.6	Melanoma* (met) Hs688(B).T	70.2	62.4
Colon ca. HCC-2998	0.0	0.1	Melanoma UACC-62	0.0	0.0
Gastric ca.* (liver met) NCI-N87	2.0	1.8	Melanoma M14	14.3	12.2
Bladder	1.4	1.1	Melanoma LOX IMVI	0.3	0.3
Trachea	0.9	0.8	Melanoma* (met) SK-MEL-5	1.1	1.2
Kidney	0.3	0.3	Adipose	1.1	1.4

Table LD. Panel 2D

Tissue Name	Rel. Exp.(%) Ag2049, Run 169484161	Tissue Name	Rel. Exp.(%) Ag2049, Run 169484161
Normal Colon	8.4	Kidney Margin 8120608	1.4
CC Well to Mod Diff (ODO3866)	12.6	Kidney Cancer 8120613	0.7
CC Margin (ODO3866)	2.7	Kidney Margin 8120614	1.0
CC Gr.2 rectosigmoid (ODO3868)	14.5	Kidney Cancer 9010320	48.6
CC Margin (ODO3868)	2.0	Kidney Margin 9010321	2.1
CC Mod Diff (ODO3920)	1.4	Normal Uterus	1.6
CC Margin (ODO3920)	2.9	Uterus Cancer 064011	2.1
CC Gr.2 ascend colon (ODO3921)	24.1	Normal Thyroid	1.3
CC Margin (ODO3921)	10.6	Thyroid Cancer 064010	0.9
CC from Partial Hepatectomy (ODO4309) Mets	39.8	Thyroid Cancer A302152	1.3
Liver Margin (ODO4309)	4.4	Thyroid Margin A302153	0.8
Colon mets to lung (OD04451-01)	24.0	Normal Breast	2.5
Lung Margin (OD04451-02)	3.1	Breast Cancer (OD04566)	1.3
Normal Prostate 6546-1	1.0	Breast Cancer (OD04590-01)	5.5
Prostate Cancer (OD04410)	4.0	Breast Cancer Mets (OD04590-03)	5.3
Prostate Margin (OD04410)	2.2	Breast Cancer Metastasis (OD04655-05)	2.2
Prostate Cancer (OD04720-01)	2.5	Breast Cancer 064006	7.5
Prostate Margin (OD04720-02)	6.5	Breast Cancer 1024	3.5
Normal Lung 061010	8.2	Breast Cancer 9100266	3.1

Lung Met to Muscle (ODO4286)	21.3	Breast Margin 9100265	5.5
Muscle Margin (ODO4286)	3.8	Breast Cancer A209073	4.5
Lung Malignant Cancer (OD03126)	23.8	Breast Margin A209073	2.1
Lung Margin (OD03126)	7.1	Normal Liver	3.3
Lung Cancer (OD04404)	38.4	Liver Cancer 064003	6.8
Lung Margin (OD04404)	9.1	Liver Cancer 1025	5.1
Lung Cancer (OD04565)	4.4	Liver Cancer 1026	7.7
Lung Margin (OD04565)	2.6	Liver Cancer 6004-T	5.4
Lung Cancer (OD04237-01)	5.1	Liver Tissue 6004-N	9.3
Lung Margin (OD04237-02)	7.9	Liver Cancer 6005-T	7.4
Ocular Mel Met to Liver (ODO4310)	0.3	Liver Tissue 6005-N	4.5
Liver Margin (ODO4310)	5.3	Normal Bladder	7.6
Melanoma Mets to Lung (OD04321)	3.3	Bladder Cancer 1023	10.4
Lung Margin (OD04321)	5.2	Bladder Cancer A302173	6.1
Normal Kidney	4.7	Bladder Cancer (OD04718-01)	29.5
Kidney Ca, Nuclear grade 2 (OD04338)	6.5	Bladder Normal Adjacent (OD04718-03)	8.7
Kidney Margin (OD04338)	2.3	Normal Ovary	2.2
Kidney Ca Nuclear grade 1/2 (OD04339)	2.4	Ovarian Cancer 064008	23.8
Kidney Margin (OD04339)	1.1	Ovarian Cancer (OD04768-07)	2.4
Kidney Ca, Clear cell type (OD04340)	4.7	Ovary Margin (OD04768-08)	5.4
Kidney Margin (OD04340)	3.2	Normal Stomach	3.4
Kidney Ca, Nuclear	23.8	Gastric Cancer	3.4

grade 3 (OD04348)		9060358	
Kidney Margin (OD04348)	1.6	Stomach Margin 9060359	2.1
Kidney Cancer (OD04622-01)	**100.0**	Gastric Cancer 9060395	17.8
Kidney Margin (OD04622-03)	0.6	Stomach Margin 9060394	4.0
Kidney Cancer (OD04450-01)	2.6	Gastric Cancer 9060397	19.8
Kidney Margin (OD04450-03)	1.8	Stomach Margin 9060396	1.6
Kidney Cancer 8120607	1.4	Gastric Cancer 064005	9.9

Table LE. Panel 3D

Tissue Name	Rel. Exp.(%) Ag2049, Run 170189502	Tissue Name	Rel. Exp.(%) Ag2049, Run 170189502
Daoy- Medulloblastoma	49.7	Ca Ski- Cervical epidermoid carcinoma (metastasis)	52.5
TE671- Medulloblastoma	0.0	ES-2- Ovarian clear cell carcinoma	0.4
D283 Med- Medulloblastoma	0.0	Ramos- Stimulated with PMA/ionomycin 6h	0.0
PFSK-1- Primitive Neuroectodermal	0.3	Ramos- Stimulated with PMA/ionomycin 14h	0.0
XF-498- CNS	4.7	MEG-01- Chronic myelogenous leukemia (megokaryoblast)	0.1
SNB-78- Glioma	**100.0**	Raji- Burkitt's lymphoma	0.0
SF-268- Glioblastoma	2.9	Daudi- Burkitt's lymphoma	0.0
T98G- Glioblastoma	66.0	U266- B-cell plasmacytoma	0.0
SK-N-SH- Neuroblastoma (metastasis)	62.4	CA46- Burkitt's lymphoma	0.0
SF-295- Glioblastoma	47.3	RL- non-Hodgkin's B-cell lymphoma	0.0
Cerebellum	0.1	JM1- pre-B-cell lymphoma	0.0
Cerebellum	0.1	Jurkat- T cell leukemia	0.0
NCI-H292- Mucoepidermoid lung carcinoma	21.6	TF-1- Erythroleukemia	0.0
DMS-114- Small cell lung cancer	0.0	HUT 78- T-cell lymphoma	0.0
DMS-79- Small cell lung cancer	0.0	U937- Histiocytic lymphoma	0.0
NCI-H146- Small cell lung cancer	0.0	KU-812- Myelogenous leukemia	0.0
NCI-H526- Small cell lung cancer	0.0	769-P- Clear cell renal carcinoma	6.9
NCI-N417- Small cell lung cancer	0.0	Caki-2- Clear cell renal carcinoma	1.3
NCI-H82- Small cell lung cancer	0.0	SW 839- Clear cell renal carcinoma	8.3
NCI-H157- Squamous cell lung cancer (metastasis)	84.1	G401- Wilms' tumor	0.0

NCI-H1155- Large cell lung cancer	0.1	Hs766T- Pancreatic carcinoma (LN metastasis)	2.1
NCI-H1299- Large cell lung cancer	5.3	CAPAN-1- Pancreatic adenocarcinoma (liver metastasis)	0.4
NCI-H727- Lung carcinoid	11.6	SU86.86- Pancreatic carcinoma (liver metastasis)	10.7
NCI-UMC-11- Lung carcinoid	0.1	BxPC-3- Pancreatic adenocarcinoma	2.6
LX-1- Small cell lung cancer	16.7	HPAC- Pancreatic adenocarcinoma	4.4
Colo-205- Colon cancer	5.1	MIA PaCa-2- Pancreatic carcinoma	1.0
KM12- Colon cancer	2.2	CFPAC-1- Pancreatic ductal adenocarcinoma	15.1
KM20L2- Colon cancer	0.7	PANC-1- Pancreatic epithelioid ductal carcinoma	6.4
NCI-H716- Colon cancer	0.6	T24- Bladder carcinma (transitional cell)	0.7
SW-48- Colon adenocarcinoma	14.8	5637- Bladder carcinoma	9.9
SW1116- Colon adenocarcinoma	0.0	HT-1197- Bladder carcinoma	1.7
LS 174T- Colon adenocarcinoma	34.2	UM-UC-3- Bladder carcinma (transitional cell)	1.1
SW-948- Colon adenocarcinoma	0.2	A204- Rhabdomyosarcoma	0.0
SW-480- Colon adenocarcinoma	2.2	HT-1080- Fibrosarcoma	1.2
NCI-SNU-5- Gastric carcinoma	4.6	MG-63- Osteosarcoma	31.9
KATO III- Gastric carcinoma	5.9	SK-LMS-1- Leiomyosarcoma (vulva)	19.2
NCI-SNU-16- Gastric carcinoma	26.4	SJRH30- Rhabdomyosarcoma (met to bone marrow)	0.0
NCI-SNU-1- Gastric carcinoma	0.2	A431- Epidermoid carcinoma	8.6
RF-1- Gastric adenocarcinoma	0.0	WM266-4- Melanoma	0.5
RF-48- Gastric adenocarcinoma	0.0	DU 145- Prostate carcinoma (brain metastasis)	0.1

MKN-45- Gastric carcinoma	0.1	MDA-MB-468- Breast adenocarcinoma	0.6
NCI-N87- Gastric carcinoma	5.4	SCC-4- Squamous cell carcinoma of tongue	0.1
OVCAR-5- Ovarian carcinoma	6.2	SCC-9- Squamous cell carcinoma of tongue	0.5
RL95-2- Uterine carcinoma	0.0	SCC-15- Squamous cell carcinoma of tongue	0.1
HelaS3- Cervical adenocarcinoma	0.7	CAL 27- Squamous cell carcinoma of tongue	9.3

Table LF. Panel 4D

Tissue Name	Rel. Exp.(%) Ag2049, Run 147506526	Tissue Name	Rel. Exp.(%) Ag2049, Run 147506526
Secondary Th1 act	0.0	HUVEC IL-1beta	0.3
Secondary Th2 act	0.0	HUVEC IFN gamma	0.3
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.3
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.6
Secondary Th2 rest	0.0	HUVEC IL-11	0.1
Secondary Tr1 rest	0.0	Lung Microvascular EC none	10.4
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	11.8
Primary Th2 act	0.0	Microvascular Dermal EC none	12.7
Primary Tr1 act	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	5.4
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	23.7
Primary Th2 rest	0.0	Small airway epithelium none	12.9
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	40.3
CD45RA CD4 lymphocyte act	6.5	Coronery artery SMC rest	**100.0**
CD45RO CD4 lymphocyte act	0.0	Coronery artery SMC TNFalpha + IL-1beta	72.2
CD8 lymphocyte act	0.0	Astrocytes rest	65.1
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	39.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.2	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	25.5
LAK cells rest	5.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	8.3
LAK cells IL-2	0.0	Liver cirrhosis	2.2

LAK cells IL-2+IL-12	0.1	Lupus kidney	0.3
LAK cells IL-2+IFN gamma	0.2	NCI-H292 none	24.7
LAK cells IL-2+ IL-18	0.1	NCI-H292 IL-4	21.5
LAK cells PMA/ionomycin	5.9	NCI-H292 IL-9	22.2
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	7.4
Two Way MLR 3 day	1.4	NCI-H292 IFN gamma	6.8
Two Way MLR 5 day	0.2	HPAEC none	0.5
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.6
PBMC rest	2.3	Lung fibroblast none	15.0
PBMC PWM	0.1	Lung fibroblast TNF alpha + IL-1 beta	14.5
PBMC PHA-L	0.3	Lung fibroblast IL-4	36.3
Ramos (B cell) none	0.0	Lung fibroblast IL-9	24.1
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	20.4
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	42.9
B lymphocytes CD40L and IL-4	0.1	Dermal fibroblast CCD1070 rest	55.5
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	34.9
EOL-1 dbcAMP PMA/ionomycin	0.1	Dermal fibroblast CCD1070 IL-1 beta	25.5
Dendritic cells none	15.7	Dermal fibroblast IFN gamma	6.6
Dendritic cells LPS	2.1	Dermal fibroblast IL-4	24.1
Dendritic cells anti-CD40	19.8	IBD Colitis 2	0.1
Monocytes rest	17.7	IBD Crohn's	0.4
Monocytes LPS	1.4	Colon	2.5
Macrophages rest	8.5	Lung	9.0
Macrophages LPS	2.9	Thymus	1.6
HUVEC none	0.6	Kidney	4.0
HUVEC starved	0.8		

Table LG. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag2049, Run 258052272	Rel. Exp.(%) Ag2049, Run 258707236	Tissue Name	Rel. Exp.(%) Ag2049, Run 258052272	Rel. Exp.(%) Ag2049, Run 258707236
Colon cancer 1	14.9	19.8	Bladder cancer NAT 2	0.1	0.1
Colon cancer NAT 1	10.6	12.3	Bladder cancer NAT 3	1.9	0.3
Colon cancer 2	24.5	24.5	Bladder cancer NAT 4	1.3	2.0
Colon cancer NAT 2	2.4	2.4	Adenocarcinoma of the prostate 1	4.5	4.1
Colon cancer 3	59.0	72.2	Adenocarcinoma of the prostate 2	0.4	0.4
Colon cancer NAT 3	4.0	4.4	Adenocarcinoma of the prostate 3	0.4	0.6
Colon malignant cancer 4	16.3	17.0	Adenocarcinoma of the prostate 4	7.3	23.8
Colon normal adjacent tissue 4	1.0	2.1	Prostate cancer NAT 5	0.5	0.5
Lung cancer 1	11.2	11.6	Adenocarcinoma of the prostate 6	0.2	0.4
Lung NAT 1	0.5	0.7	Adenocarcinoma of the prostate 7	0.5	0.4
Lung cancer 2	18.0	20.3	Adenocarcinoma of the prostate 8	0.2	0.3
Lung NAT 2	0.6	0.7	Adenocarcinoma of the prostate 9	3.7	3.7
Squamous cell carcinoma 3	15.3	14.4	Prostate cancer NAT 10	0.2	0.3
Lung NAT 3	0.4	0.6	Kidney cancer 1	**100.0**	**100.0**
metastatic melanoma 1	1.1	1.2	KidneyNAT 1	1.7	1.6

Melanoma 2	2.5	2.7	Kidney cancer 2	17.7	22.7
Melanoma 3	1.1	1.5	Kidney NAT 2	2.1	2.6
metastatic melanoma 4	5.0	5.7	Kidney cancer 3	13.2	14.5
metastatic melanoma 5	4.4	10.9	Kidney NAT 3	0.5	0.7
Bladder cancer 1	1.4	1.5	Kidney cancer 4	9.6	9.6
Bladder cancer NAT 1	0.0	0.0	Kidney NAT 4	0.5	0.7
Bladder cancer 2	1.9	2.5			

General_screening_panel_v1.4 Summary: Ag2049 Highest expression of the CG95861-01 gene is seen in melanoma (CT=17.5). Overall, expression is much higher in cancer cell lines than in normal tissues. This pattern is also seen in Panels 1.3D and 2D. Please see Panel 2D for discussion of utility of this gene in cancer.

5   Panel 1.3D Summary: Ag2049 Two experiments with the same probe and primer set produce results that are in excellent agreement. Overall, the expression of this gene in this panel is largely limited to samples derived from cancer cell lines. In particular there is a strong association (8 of 9) with expression of this gene prodcut, a transforming growth factor-beta induced protein IG-H3

10   precursor (BETA IG-H3) homolog, and cell lines derived from CNS cancer tissue, with highest expression of the CG95861-01 gene in cell lines derived from brain cancer (CTs=22-23.7). In addition, there is little expression in the normal brain samples when compared to the CNS derived cell lines. This putative BIGH3 is also expressed in a number of other cell lines derived from cancer tissues including melanoma, ovarian,

15   breast, lung and renal cancers. Relatively low expression is observed in RNA samples corresponding to normal counterparts to these cancer cell lines. Please see Panel 2D for discussion of utility of this gene in cancer.

          Panel 2D Summary: Ag2049 Highest expression of this putative BIG-H3 protein is seen in kidney cancer (CT=22). In addition, expression of this gene produt is seen in a

20   number of cancer tissues, but not adjacent uninvolved sample. These include samples from

gastric, bladder, kidney, lung and colon cancers. This suggests that the expression of BIGH3 might be associated with cancer.

Beta ig-h3 (BIGH3), was identified originally as a novel gene induced in a human adenocarcinoma cell line after treatment with transforming growth factor-beta (Skonier et

5   al. DNA Cell Biol 1992 Sep;11(7):511-22). Most notable, with respect to potential roles in cancer biology, is a follow-up report by Skonier et al. in which it was reported that soluble BIGH3 was found to be capable of inhibiting the attachment of A549 lung carcinoma, HeLa cervical carcinoma, and WI-38 fibroblast cells in an in vitro adhesion assay. Moreover, Skonier et al reported that ectopic overexpression of BIGH3 was found to be

10   capable of suppressing the growth of CHO cells in nude mice (DNA Cell Biol 1994 Jun;13(6):571-84). Finally, Skonier et al mapped BIGH3 to human chromosome 5q31, a region frequently deleted in preleukemic myelodysplasia and leukemias, providing casual support to the notion that BIGH3 is a tumor suppressor.

Our data indicates that BIGH3 is unlikely to function as a tumor growth

15   suppressor, but rather as a pro-active effector of tumor growth and perhaps resistance to cytotoxic therapy. BIGH3 (gbh_m77349) was identified in a GeneCalling analysis (Shimkets et al. Nat Biotechnol 1999 Aug;17(8):798-803) of differential gene expression comparison between MCF-7 cells (ER positive,, p53 positive, vimentin negative, noninvasive) and MCF-7/Adr (estrogen receptor negative, p53 negative, vimentin positive,

20   invasive and hormone resistant) cells (Fairchild et al. Cancer Res 1987 Oct 1;47(19):5141-8). MCF-7 Cells were derived from MCF-7 cells by virtue of their relative resistance to the front-line therapeutic agent for patients with breast cancer, adriamycin (doxorubicin), a DNA intercalating agent. In the GeneCalling analysis BIGH3 was found to be approximately 100-fold upregulated in MCF-7/Adr cells relative to MCF-7 cells.

25   Data obtained from real-time quantitative polymerase chain reaction (RTQ_PCR) analysis supports a pro-active role for BIGH3 in tumor etiology and/or progression. By RTQ-PCR we find that BIGH3 is expressed at high levels by most tumor cell lines relative to normal tissues or origins (see Panel 1.3D) and is frequently overexpressed in tumor tissues relative to histopathologically normal tissues obtained from the surgical margin

30   adjacent to the tumor (see Panel 2D). This is most notable for clear cell carcinomas of the kidney, colon adenocarcinomas, non-small cell carcinomas of the lung, and carcinomas of the stomach. The striking and consistently high expression by cell lines derived form

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gliomas, astrocytomas and mixed glioma/astrocytomas strongly supports the role in the development and/or progression of malignancies of the CNS.

Six autosomal dominant corneal dystrophies are caused by mutations in the TGFBI (BIGH3) gene on chromosome 5q31: three types of lattice corneal dystrophy (LCD), including type I and type IIIA, granular, Avellino (ACD), and Reis-Bucklers. The embryonic expression of the mouse ortholog in Bigh3 is observed in the mesenchyme of the first and second branchial arches as early as dpc 11.5 and is particularly strong in the mesenchyme of numerous tissues throughout all the development stages (Biochem Biophys Res Commun 2000 Aug 2;274(2):267-74). Mesenchymal cells are characterized by high growth rate, motility and invasion. The strong expression of this gene by most tumor cell lines in Panel 1.3D indicate that it is part of the epithelial to mesenchymal switch that tumor cells undergo during tumorogenic cellular transformation. Therefore, we postulate that this gene product has a role in tumor invasion, cell migration and growth, metastasis. Because of its activity and overexpression in many tumor types in panel 2D, therapeutic targeting of thsi gene product with a human monoclonal antibody is anticipated to limit or block the extent of tumor cell migration, invasion, growth and metastasis, preferably in gastric and colon, kidney, lung, bladder and ovarian tumors.

Panel 3D Summary: Ag2049 Highest expression of the CG95861-01 gene is seen in a glioma cell line (CT=23.6). Expression in this panel confirms expression of this gene product in cancer cell lines and suggests its central role in cell survival and growth. Please see Panel 2D for detailed discussion of utility of this gene in cancer.

Panel 4D Summary: Ag2049 The expression of the CG95861-01 gene, which encodes a putative BIGH3 molecule, is seen in many cells involved in the immune system including endothelial cells, astrocytes, fibroblasts and monocytes, macrophages and dendritic cells. Highest expression is seen in resting coronary artery smooth muscle cells (CT=22.2). Expression in a cluster of samples derived from cells in the lung and skin suggest that this gene product may be involved in pathological and inflammatory conditions of the lung and skin, including psoriasis, asthma, emphysema and allergy.

general oncology screening panel_v_2.4 Summary: Ag2049 Two experiments with the same probe and primer set produce results that are in excellent agreement. Highest expression of the CG95861-01 gene is seen in kidney cancer (CTs=21-23). This expression is in agreement with expression in previous panels. Significant levels of expression are also seen in colon, lung and bladder cancers when compared to expression

in the normal adjacent tissue. This gene is also expressed at a moderate level in the melanoma samples in this panel. Please see Panel 2D for additional discussion of utility of this gene in cancer. [sedinger, 18-Mar-02]

M. CG96412-01: diphthamide synthesis protein

Expression of gene CG96412-01 was assessed using the primer-probe sets Ag1985 and Ag4055, described in Tables MA and MB. Results of the RTQ-PCR runs are shown in Tables MC, MD, ME, MF, MG, MH and MI.

Table MA. Probe Name Ag1985

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-agttaatcaacacccacatgct-3'	22	8165	176
Probe	TET-5'-ccccgaggtcttgcagattaaaacg-3'-TAMRA	25	8119	177
Reverse	5'-tggaacccagaagcaagtg-3'	19	8100	178

Table MB. Probe Name Ag4055

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgcctctgcaagacaagaa-3'	20	3917	179
Probe	TET-5'-tttctggaagatcacaccaactcctg-3'-TAMRA	26	3947	180
Reverse	5'-tccctggcaactatgtctga-3'	20	3981	181

Table MC. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag1985, Run 225403959	Tissue Name	Rel. Exp.(%) Ag1985, Run 225403959
110967 COPD-F	6.9	112427 Match Control Psoriasis-F	45.7
110980 COPD-F	10.8	112418 Psoriasis-M	11.1
110968 COPD-M	5.5	112723 Match Control Psoriasis-M	5.1
110977 COPD-M	29.1	112419 Psoriasis-M	7.6
110989 Emphysema-F	13.4	112424 Match Control Psoriasis-M	5.8
110992 Emphysema-F	4.5	112420 Psoriasis-M	21.6
110993 Emphysema-F	5.4	112425 Match Control Psoriasis-M	25.9
110994 Emphysema-F	3.2	104689 (MF) OA Bone-Backus	6.5
110995 Emphysema-F	14.3	104690 (MF) Adj "Normal" Bone-Backus	6.3
110996 Emphysema-F	5.6	104691 (MF) OA Synovium-Backus	3.8
110997 Asthma-M	2.0	104692 (BA) OA Cartilage-Backus	2.6
111001 Asthma-F	5.7	104694 (BA) OA Bone-Backus	3.1
111002 Asthma-F	9.5	104695 (BA) Adj "Normal" Bone-Backus	3.0
111003 Atopic Asthma-F	11.3	104696 (BA) OA Synovium-Backus	2.0
111004 Atopic Asthma-F	10.7	104700 (SS) OA Bone-Backus	7.3
111005 Atopic Asthma-F	6.5	104701 (SS) Adj "Normal" Bone-Backus	6.3
111006 Atopic Asthma-F	1.2	104702 (SS) OA Synovium-Backus	5.4
111417 Allergy-M	4.5	117093 OA Cartilage Rep7	8.6
112347 Allergy-M	1.3	112672 OA Bone5	7.4
112349 Normal Lung-F	1.6	112673 OA Synovium5	1.7

112357 Normal Lung-F	**100.0**	112674 OA Synovial Fluid cells5	1.8
112354 Normal Lung-M	55.9	117100 OA Cartilage Rep14	1.7
112374 Crohns-F	7.3	112756 OA Bone9	7.0
112389 Match Control Crohns-F	8.4	112757 OA Synovium9	4.3
112375 Crohns-F	6.4	112758 OA Synovial Fluid Cells9	2.4
112732 Match Control Crohns-F	1.1	117125 RA Cartilage Rep2	11.2
112725 Crohns-M	2.5	113492 Bone2 RA	23.5
112387 Match Control Crohns-M	5.0	113493 Synovium2 RA	6.4
112378 Crohns-M	2.7	113494 Syn Fluid Cells RA	18.7
112390 Match Control Crohns-M	8.0	113499 Cartilage4 RA	15.3
112726 Crohns-M	11.7	113500 Bone4 RA	20.9
112731 Match Control Crohns-M	10.8	113501 Synovium4 RA	10.9
112380 Ulcer Col-F	8.7	113502 Syn Fluid Cells4 RA	6.5
112734 Match Control Ulcer Col-F	12.0	113495 Cartilage3 RA	6.4
112384 Ulcer Col-F	38.2	113496 Bone3 RA	13.4
112737 Match Control Ulcer Col-F	8.5	113497 Synovium3 RA	5.7
112386 Ulcer Col-F	1.1	113498 Syn Fluid Cells3 RA	10.4
112738 Match Control Ulcer Col-F	0.5	117106 Normal Cartilage Rep20	1.4
112381 Ulcer Col-M	0.6	113663 Bone3 Normal	2.1
112735 Match Control Ulcer Col-M	5.4	113664 Synovium3 Normal	0.7
112382 Ulcer Col-M	5.4	113665 Syn Fluid Cells3 Normal	0.3
112394 Match Control Ulcer Col-M	0.2	117107 Normal Cartilage Rep22	2.9
112383 Ulcer Col-M	51.4	113667 Bone4 Normal	14.6
112736 Match Control Ulcer Col-M	1.2	113668 Synovium4 Normal	18.7

| 112423 Psoriasis-F | 36.6 | 113669 Syn Fluid Cells4 Normal | 28.5 |

Table MD. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag1985, Run 207794788	Tissue Name	Rel. Exp.(%) Ag1985, Run 207794788
AD 1 Hippo	14.3	Control (Path) 3 Temporal Ctx	2.1
AD 2 Hippo	27.4	Control (Path) 4 Temporal Ctx	19.9
AD 3 Hippo	4.4	AD 1 Occipital Ctx	8.0
AD 4 Hippo	16.3	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	45.4	AD 3 Occipital Ctx	10.4
AD 6 Hippo	49.7	AD 4 Occipital Ctx	5.8
Control 2 Hippo	25.3	AD 5 Occipital Ctx	70.2
Control 4 Hippo	51.1	AD 6 Occipital Ctx	42.9
Control (Path) 3 Hippo	5.0	Control 1 Occipital Ctx	5.0
AD 1 Temporal Ctx	11.3	Control 2 Occipital Ctx	22.5
AD 2 Temporal Ctx	21.3	Control 3 Occipital Ctx	7.1
AD 3 Temporal Ctx	2.5	Control 4 Occipital Ctx	4.5
AD 4 Temporal Ctx	19.3	Control (Path) 1 Occipital Ctx	**100.0**
AD 5 Inf Temporal Ctx	38.2	Control (Path) 2 Occipital Ctx	7.7
AD 5 SupTemporal Ctx	50.3	Control (Path) 3 Occipital Ctx	0.0
AD 6 Inf Temporal Ctx	34.6	Control (Path) 4 Occipital Ctx	6.5
AD 6 Sup Temporal Ctx	34.2	Control 1 Parietal Ctx	6.3
Control 1 Temporal Ctx	4.8	Control 2 Parietal Ctx	33.9
Control 2 Temporal Ctx	4.5	Control 3 Parietal Ctx	10.8
Control 3 Temporal Ctx	10.7	Control (Path) 1 Parietal Ctx	59.0
Control 4 Temporal	0.0	Control (Path) 2	5.6

Ctx		Parietal Ctx	
Control (Path) 1 Temporal Ctx	21.0	Control (Path) 3 Parietal Ctx	0.0
Control (Path) 2 Temporal Ctx	20.3	Control (Path) 4 Parietal Ctx	24.0

Table ME. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4055, Run 218713249	Tissue Name	Rel. Exp.(%) Ag4055, Run 218713249
Adipose	14.3	Renal ca. TK-10	9.7
Melanoma* Hs688(A).T	10.9	Bladder	6.7
Melanoma* Hs688(B).T	10.2	Gastric ca. (liver met.) NCI-N87	10.8
Melanoma* M14	11.6	Gastric ca. KATO III	15.0
Melanoma* LOXIMVI	6.6	Colon ca. SW-948	3.3
Melanoma* SK-MEL-5	6.3	Colon ca. SW480	11.7
Squamous cell carcinoma SCC-4	2.7	Colon ca.* (SW480 met) SW620	11.0
Testis Pool	7.0	Colon ca. HT29	2.5
Prostate ca.* (bone met) PC-3	6.9	Colon ca. HCT-116	11.9
Prostate Pool	6.2	Colon ca. CaCo-2	9.2
Placenta	9.1	Colon cancer tissue	4.9
Uterus Pool	5.0	Colon ca. SW1116	3.8
Ovarian ca. OVCAR-3	6.4	Colon ca. Colo-205	2.2
Ovarian ca. SK-OV-3	6.8	Colon ca. SW-48	1.1
Ovarian ca. OVCAR-4	1.9	Colon Pool	16.2
Ovarian ca. OVCAR-5	11.7	Small Intestine Pool	36.1
Ovarian ca. IGROV-1	6.2	Stomach Pool	9.2
Ovarian ca. OVCAR-8	10.2	Bone Marrow Pool	10.0
Ovary	7.8	Fetal Heart	6.5
Breast ca. MCF-7	9.0	Heart Pool	6.2
Breast ca. MDA-MB-231	12.2	Lymph Node Pool	21.5
Breast ca. BT 549	12.9	Fetal Skeletal Muscle	4.3
Breast ca. T47D	25.5	Skeletal Muscle Pool	6.8
Breast ca. MDA-N	15.6	Spleen Pool	14.3
Breast Pool	13.8	Thymus Pool	9.7
Trachea	8.4	CNS cancer	8.2

		(glio/astro) U87-MG	
Lung	19.8	CNS cancer (glio/astro) U-118-MG	29.3
Fetal Lung	50.0	CNS cancer (neuro;met) SK-N-AS	7.6
Lung ca. NCI-N417	4.3	CNS cancer (astro) SF-539	5.2
Lung ca. LX-1	11.1	CNS cancer (astro) SNB-75	13.7
Lung ca. NCI-H146	6.4	CNS cancer (glio) SNB-19	9.1
Lung ca. SHP-77	25.7	CNS cancer (glio) SF-295	26.1
Lung ca. A549	9.0	Brain (Amygdala) Pool	7.2
Lung ca. NCI-H526	1.7	Brain (cerebellum)	**100.0**
Lung ca. NCI-H23	20.2	Brain (fetal)	30.6
Lung ca. NCI-H460	8.9	Brain (Hippocampus) Pool	12.0
Lung ca. HOP-62	9.9	Cerebral Cortex Pool	12.7
Lung ca. NCI-H522	6.7	Brain (Substantia nigra) Pool	10.4
Liver	0.9	Brain (Thalamus) Pool	14.9
Fetal Liver	6.3	Brain (whole)	16.0
Liver ca. HepG2	3.2	Spinal Cord Pool	10.4
Kidney Pool	34.4	Adrenal Gland	18.9
Fetal Kidney	14.1	Pituitary gland Pool	50.7
Renal ca. 786-0	4.2	Salivary Gland	5.6
Renal ca. A498	1.6	Thyroid (female)	7.6
Renal ca. ACHN	8.8	Pancreatic ca. CAPAN2	6.2
Renal ca. UO-31	2.9	Pancreas Pool	17.7

Table MF. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag1985, Run 147745294	Tissue Name	Rel. Exp.(%) Ag1985, Run 147745294
Liver adenocarcinoma	6.0	Kidney (fetal)	7.8
Pancreas	0.7	Renal ca. 786-0	2.2
Pancreatic ca. CAPAN 2	1.9	Renal ca. A498	4.4
Adrenal gland	31.6	Renal ca. RXF 393	0.7
Thyroid	2.3	Renal ca. ACHN	6.6
Salivary gland	2.0	Renal ca. UO-31	0.0
Pituitary gland	**100.0**	Renal ca. TK-10	2.8
Brain (fetal)	0.0	Liver	0.7
Brain (whole)	4.6	Liver (fetal)	3.8
Brain (amygdala)	13.5	Liver ca. (hepatoblast) HepG2	0.8
Brain (cerebellum)	0.0	Lung	4.9
Brain (hippocampus)	24.1	Lung (fetal)	21.9
Brain (substantia nigra)	2.5	Lung ca. (small cell) LX-1	4.2
Brain (thalamus)	1.6	Lung ca. (small cell) NCI-H69	8.7
Cerebral Cortex	21.6	Lung ca. (s.cell var.) SHP-77	24.8
Spinal cord	12.0	Lung ca. (large cell)NCI-H460	7.0
glio/astro U87-MG	3.9	Lung ca. (non-sm. cell) A549	3.2
glio/astro U-118-MG	20.7	Lung ca. (non-s.cell) NCI-H23	12.2
astrocytoma SW1783	3.5	Lung ca. (non-s.cell) HOP-62	5.8
neuro*; met SK-N-AS	4.8	Lung ca. (non-s.cl) NCI-H522	4.9
astrocytoma SF-539	2.2	Lung ca. (squam.) SW 900	3.0
astrocytoma SNB-75	15.1	Lung ca. (squam.) NCI-H596	0.0
glioma SNB-19	6.4	Mammary gland	8.5
glioma U251	3.2	Breast ca.* (pl.ef) MCF-7	9.4
glioma SF-295	6.7	Breast ca.* (pl.ef)	6.7

		MDA-MB-231	
Heart (fetal)	17.6	Breast ca.* (pl.ef) T47D	8.6
Heart	1.6	Breast ca. BT-549	10.7
Skeletal muscle (fetal)	41.2	Breast ca. MDA-N	12.2
Skeletal muscle	0.0	Ovary	31.2
Bone marrow	0.8	Ovarian ca. OVCAR-3	1.6
Thymus	2.9	Ovarian ca. OVCAR-4	0.0
Spleen	0.5	Ovarian ca. OVCAR-5	4.8
Lymph node	3.2	Ovarian ca. OVCAR-8	6.6
Colorectal	13.3	Ovarian ca. IGROV-1	0.0
Stomach	0.9	Ovarian ca.* (ascites) SK-OV-3	2.2
Small intestine	0.0	Uterus	4.3
Colon ca. SW480	5.7	Placenta	0.0
Colon ca.* SW620(SW480 met)	1.5	Prostate	2.0
Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	0.8
Colon ca. HCT-116	1.4	Testis	14.6
Colon ca. CaCo-2	2.6	Melanoma Hs688(A).T	3.2
Colon ca. tissue(ODO3866)	19.3	Melanoma* (met) Hs688(B).T	7.9
Colon ca. HCC-2998	19.5	Melanoma UACC-62	4.3
Gastric ca.* (liver met) NCI-N87	9.7	Melanoma M14	1.6
Bladder	0.0	Melanoma LOX IMVI	0.7
Trachea	18.3	Melanoma* (met) SK-MEL-5	1.6
Kidney	1.8	Adipose	55.1

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Table MG. Panel 2D

Tissue Name	Rel. Exp.(%) Ag1985, Run 147745405	Tissue Name	Rel. Exp.(%) Ag1985, Run 147745405
Normal Colon	84.7	Kidney Margin 8120608	20.7
CC Well to Mod Diff (ODO3866)	12.3	Kidney Cancer 8120613	1.2
CC Margin (ODO3866)	11.1	Kidney Margin 8120614	12.0
CC Gr.2 rectosigmoid (ODO3868)	1.6	Kidney Cancer 9010320	46.3
CC Margin (ODO3868)	2.1	Kidney Margin 9010321	50.7
CC Mod Diff (ODO3920)	4.0	Normal Uterus	12.0
CC Margin (ODO3920)	5.3	Uterus Cancer 064011	**100.0**
CC Gr.2 ascend colon (ODO3921)	30.8	Normal Thyroid	1.4
CC Margin (ODO3921)	11.4	Thyroid Cancer 064010	8.3
CC from Partial Hepatectomy (ODO4309) Mets	10.0	Thyroid Cancer A302152	14.1
Liver Margin (ODO4309)	3.0	Thyroid Margin A302153	6.1
Colon mets to lung (OD04451-01)	7.3	Normal Breast	87.1
Lung Margin (OD04451-02)	6.6	Breast Cancer (OD04566)	6.3
Normal Prostate 6546-1	5.2	Breast Cancer (OD04590-01)	13.8
Prostate Cancer (OD04410)	39.0	Breast Cancer Mets (OD04590-03)	12.2
Prostate Margin (OD04410)	27.7	Breast Cancer Metastasis (OD04655-05)	11.5
Prostate Cancer (OD04720-01)	17.2	Breast Cancer 064006	1.6
Prostate Margin (OD04720-02)	62.4	Breast Cancer 1024	22.5
Normal Lung 061010	29.1	Breast Cancer 9100266	11.3

Lung Met to Muscle (ODO4286)	5.9	Breast Margin 9100265	10.4
Muscle Margin (ODO4286)	11.3	Breast Cancer A209073	9.2
Lung Malignant Cancer (OD03126)	13.0	Breast Margin A209073	13.7
Lung Margin (OD03126)	30.6	Normal Liver	0.0
Lung Cancer (OD04404)	8.7	Liver Cancer 064003	1.5
Lung Margin (OD04404)	54.3	Liver Cancer 1025	11.0
Lung Cancer (OD04565)	5.6	Liver Cancer 1026	1.7
Lung Margin (OD04565)	14.9	Liver Cancer 6004-T	9.0
Lung Cancer (OD04237-01)	9.8	Liver Tissue 6004-N	1.9
Lung Margin (OD04237-02)	68.3	Liver Cancer 6005-T	1.1
Ocular Mel Met to Liver (ODO4310)	3.3	Liver Tissue 6005-N	1.0
Liver Margin (ODO4310)	12.9	Normal Bladder	15.4
Melanoma Mets to Lung (OD04321)	8.9	Bladder Cancer 1023	9.2
Lung Margin (OD04321)	25.9	Bladder Cancer A302173	4.6
Normal Kidney	45.1	Bladder Cancer (OD04718-01)	25.9
Kidney Ca, Nuclear grade 2 (OD04338)	6.7	Bladder Normal Adjacent (OD04718-03)	97.9
Kidney Margin (OD04338)	26.1	Normal Ovary	20.6
Kidney Ca Nuclear grade 1/2 (OD04339)	12.9	Ovarian Cancer 064008	30.6
Kidney Margin (OD04339)	15.3	Ovarian Cancer (OD04768-07)	13.0
Kidney Ca, Clear cell type (OD04340)	17.2	Ovary Margin (OD04768-08)	74.2
Kidney Margin (OD04340)	54.0	Normal Stomach	24.0
Kidney Ca, Nuclear	9.4	Gastric Cancer	2.2

grade 3 (OD04348)		9060358	
Kidney Margin (OD04348)	11.3	Stomach Margin 9060359	6.9
Kidney Cancer (OD04622-01)	18.2	Gastric Cancer 9060395	7.2
Kidney Margin (OD04622-03)	4.9	Stomach Margin 9060394	22.4
Kidney Cancer (OD04450-01)	9.8	Gastric Cancer 9060397	11.9
Kidney Margin (OD04450-03)	13.0	Stomach Margin 9060396	0.6
Kidney Cancer 8120607	3.5	Gastric Cancer 064005	24.8

Table MH. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag1985, Run 225428479	Rel. Exp.(%) Ag4055, Run 171620013	Tissue Name	Rel. Exp.(%) Ag1985, Run 225428479	Rel. Exp.(%) Ag4055, Run 171620013
Secondary Th1 act	1.7	7.0	HUVEC IL-1beta	0.2	4.3
Secondary Th2 act	3.3	11.1	HUVEC IFN gamma	0.9	6.0
Secondary Tr1 act	2.4	16.7	HUVEC TNF alpha + IFN gamma	0.9	2.8
Secondary Th1 rest	1.3	2.6	HUVEC TNF alpha + IL4	0.4	4.5
Secondary Th2 rest	0.7	2.9	HUVEC IL-11	0.1	1.6
Secondary Tr1 rest	0.5	4.4	Lung Microvascular EC none	0.5	9.3
Primary Th1 act	6.8	14.8	Lung Microvascular EC TNFalpha + IL-1beta	0.8	6.1
Primary Th2 act	10.8	21.2	Microvascular Dermal EC none	0.2	2.1
Primary Tr1 act	6.5	17.3	Microsvasular Dermal EC TNFalpha + IL-1beta	0.8	4.1
Primary Th1 rest	0.3	1.4	Bronchial epithelium TNFalpha + IL1beta	0.7	9.4
Primary Th2 rest	0.7	2.8	Small airway epithelium none	0.2	1.9
Primary Tr1 rest	1.8	4.7	Small airway epithelium TNFalpha + IL-1beta	0.0	5.8
CD45RA CD4 lymphocyte act	1.3	6.3	Coronery artery SMC rest	0.2	3.6
CD45RO CD4 lymphocyte act	1.5	13.9	Coronery artery SMC TNFalpha + IL-1beta	0.2	2.3

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CD8 lymphocyte act	1.7	8.4	Astrocytes rest	0.3	2.1
Secondary CD8 lymphocyte rest	2.9	7.1	Astrocytes TNFalpha + IL-1beta	0.2	2.1
Secondary CD8 lymphocyte act	1.2	3.8	KU-812 (Basophil) rest	0.0	3.8
CD4 lymphocyte none	1.4	7.8	KU-812 (Basophil) PMA/ionomycin	2.5	6.9
2ry Th1/Th2/Tr1_anti-CD95 CH11	1.3	8.7	CCD1106 (Keratinocytes) none	0.6	5.3
LAK cells rest	8.2	16.5	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	1.6	7.8
LAK cells IL-2	0.4	4.4	Liver cirrhosis	1.3	4.1
LAK cells IL-2+IL-12	0.9	8.1	NCI-H292 none	1.1	3.3
LAK cells IL-2+IFN gamma	1.2	4.4	NCI-H292 IL-4	1.5	6.6
LAK cells IL-2+ IL-18	1.5	7.4	NCI-H292 IL-9	1.2	4.0
LAK cells PMA/ionomycin	**100.0**	**100.0**	NCI-H292 IL-13	1.3	5.6
NK Cells IL-2 rest	0.8	14.4	NCI-H292 IFN gamma	1.7	4.4
Two Way MLR 3 day	1.0	12.1	HPAEC none	0.4	3.7
Two Way MLR 5 day	2.4	4.7	HPAEC TNF alpha + IL-1 beta	1.3	9.0
Two Way MLR 7 day	1.4	3.0	Lung fibroblast none	0.8	7.2
PBMC rest	0.7	3.8	Lung fibroblast TNF alpha + IL-1 beta	1.4	3.3
PBMC PWM	2.9	11.0	Lung fibroblast IL-4	0.8	3.7
PBMC PHA-L	1.2	4.9	Lung fibroblast IL-9	0.7	7.1
Ramos (B cell) none	0.2	1.1	Lung fibroblast IL-13	0.8	6.3
Ramos (B cell) ionomycin	0.3	2.2	Lung fibroblast IFN gamma	2.2	6.2

B lymphocytes PWM	2.5	5.4	Dermal fibroblast CCD1070 rest	0.9	5.0
B lymphocytes CD40L and IL-4	2.4	6.9	Dermal fibroblast CCD1070 TNF alpha	1.4	8.5
EOL-1 dbcAMP	0.1	6.6	Dermal fibroblast CCD1070 IL-1 beta	1.0	4.3
EOL-1 dbcAMP PMA/ionomycin	6.3	9.0	Dermal fibroblast IFN gamma	0.9	3.6
Dendritic cells none	2.2	6.1	Dermal fibroblast IL-4	1.3	5.2
Dendritic cells LPS	1.0	4.6	Dermal Fibroblasts rest	0.6	3.6
Dendritic cells anti-CD40	2.4	9.3	Neutrophils TNFa+LPS	9.6	7.4
Monocytes rest	1.0	8.8	Neutrophils rest	1.4	5.0
Monocytes LPS	6.2	9.2	Colon	0.7	2.1
Macrophages rest	1.6	6.6	Lung	2.9	2.8
Macrophages LPS	5.0	7.3	Thymus	5.2	7.9
HUVEC none	0.6	5.6	Kidney	39.8	17.0
HUVEC starved	0.4	5.1			

Table MI. Panel 4D

Tissue Name	Rel. Exp.(%) Ag1985, Run 162350943	Tissue Name	Rel. Exp.(%) Ag1985, Run 162350943
Secondary Th1 act	1.0	HUVEC IL-1beta	0.3
Secondary Th2 act	8.2	HUVEC IFN gamma	0.9
Secondary Tr1 act	7.0	HUVEC TNF alpha + IFN gamma	0.3
Secondary Th1 rest	1.1	HUVEC TNF alpha + IL4	0.2
Secondary Th2 rest	0.9	HUVEC IL-11	0.0
Secondary Tr1 rest	1.5	Lung Microvascular EC none	0.4
Primary Th1 act	14.2	Lung Microvascular EC TNFalpha + IL-1beta	1.1
Primary Th2 act	15.4	Microvascular Dermal EC none	1.2
Primary Tr1 act	11.0	Microsvasular Dermal EC TNFalpha + IL-1beta	0.8
Primary Th1 rest	2.7	Bronchial epithelium TNFalpha + IL1beta	0.6
Primary Th2 rest	2.0	Small airway epithelium none	0.5
Primary Tr1 rest	1.2	Small airway epithelium TNFalpha + IL-1beta	2.6
CD45RA CD4 lymphocyte act	1.4	Coronery artery SMC rest	1.1
CD45RO CD4 lymphocyte act	0.9	Coronery artery SMC TNFalpha + IL-1beta	0.3
CD8 lymphocyte act	1.4	Astrocytes rest	1.8
Secondary CD8 lymphocyte rest	2.4	Astrocytes TNFalpha + IL-1beta	0.5
Secondary CD8 lymphocyte act	2.2	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.9	KU-812 (Basophil) PMA/ionomycin	5.7
2ry Th1/Th2/Tr1_anti-CD95 CH11	3.3	CCD1106 (Keratinocytes) none	1.2
LAK cells rest	10.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	1.7
LAK cells IL-2	0.7	Liver cirrhosis	3.2

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LAK cells IL-2+IL-12	1.7	Lupus kidney	0.8
LAK cells IL-2+IFN gamma	1.7	NCI-H292 none	1.3
LAK cells IL-2+ IL-18	1.9	NCI-H292 IL-4	2.6
LAK cells PMA/ionomycin	**100.0**	NCI-H292 IL-9	2.1
NK Cells IL-2 rest	1.1	NCI-H292 IL-13	0.9
Two Way MLR 3 day	2.4	NCI-H292 IFN gamma	3.9
Two Way MLR 5 day	2.0	HPAEC none	0.3
Two Way MLR 7 day	0.2	HPAEC TNF alpha + IL-1 beta	0.8
PBMC rest	1.3	Lung fibroblast none	0.5
PBMC PWM	5.1	Lung fibroblast TNF alpha + IL-1 beta	0.5
PBMC PHA-L	2.7	Lung fibroblast IL-4	0.6
Ramos (B cell) none	0.3	Lung fibroblast IL-9	1.7
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.3
B lymphocytes PWM	11.1	Lung fibroblast IFN gamma	3.9
B lymphocytes CD40L and IL-4	1.8	Dermal fibroblast CCD1070 rest	1.3
EOL-1 dbcAMP	0.7	Dermal fibroblast CCD1070 TNF alpha	3.8
EOL-1 dbcAMP PMA/ionomycin	7.7	Dermal fibroblast CCD1070 IL-1 beta	1.9
Dendritic cells none	3.0	Dermal fibroblast IFN gamma	3.1
Dendritic cells LPS	1.9	Dermal fibroblast IL-4	1.9
Dendritic cells anti-CD40	4.6	IBD Colitis 2	0.0
Monocytes rest	0.6	IBD Crohn's	1.1
Monocytes LPS	6.1	Colon	4.0
Macrophages rest	1.7	Lung	8.2
Macrophages LPS	8.7	Thymus	1.5
HUVEC none	0.0	Kidney	2.2
HUVEC starved	0.5		

AI_comprehensive panel_v1.0 Summary: Ag1985 Expression of the CG96412-01 gene, which encodes a putative dipthamide synthesis protein, is highest in lung (CT=29.3). This gene is expressed widely in this panel, confirming its presence in tissues

involved in the immune response. Please see Panel 4.1D for discussion of utility of this gene in inflammation.

CNS_neurodegeneration_v1.0 Summary: Ag1985 This gene appears to be slightly upregulated in the temporal cortex of patients suffering from Alzheimer's disease.

5   Thus, modulation of the expression or function of this gene may decrease neuronal death and be of use in the treatment of this disease. Results from a second experiment with the probe and primer set Ag4055 are not included. The amp plot indicates there were experimental difficulties with this run.

General_screening_panel_v1.4 Summary: Ag4055 The CG96412-01 gene is

10   widely expressed in this panel, with highest expression in the cerebellum (CT=28.13). The high levels of expression in the cerebellum suggest that this gene product may be a useful and specific target of drugs for the treatment of CNS disorders that have this brain region as the site of pathology, such as autism and the ataxias. Moderate levels of expression are seen across the CNS, including the amygdala, hippocampus, cerebral cortex, substantia

15   nigra and thalamus. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal

20   muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic function and that disregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

Panel 1.3D Summary: Ag1985 Expression of the CG96412-01 gene is highest in

25   the pituitary (CT=31), with low but significant levels also evident in the amygdala, cerebellum, cerebral cortex and spinal cord. Please see the previous panels for discussion of utility of this gene in the CNS.

Among other tissues with metabolic function, this gene is expressed at low levels in adipose, adrenal gland, and fetal skeletal muscle and heart. This expression suggests

30   that this gene product may play a role in normal neuroendocrine and metabolic function and that disregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes. In addition, expression of this gene

product could be used to differentiate between fetal skeletal muscle (CT=32.4) and adult skeletal muscle (CT=40).

Panel 2D Summary: Ag1985 The CG96412-01 gene is most highly expressed in uterine cancer (CT=31.1). In addition, higher levels of expression are seen in normal bladder, ovary, lung, kidney, and prostate when compared to expression in the corresponding adjacent tumor. Thus, expression of this gene could be used as a marker of these tissues. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of bladder, ovary, lung, kidney, uterine and prostate cancers.

Panel 4.1D Summary: Ag1985/Ag4055 Two experiments with two different probe and primer sets produce results that are in excellent agreement. The CG96412-01 gene is widely expressed in this panel, with highest expression in LAK cells treated with PMA and ionomycin (CTs=27-27.6). Lower levels of induction are seen in macrophages and monocytes after treatment with LPS and in EOL cells (eosinophil cell line) after treatment with PMA/ionomycin. Thus, this transcript encodes a protein that appears to be expressed in response to activation and may be involved in the immune function or proliferation of LAK cells, macrophages and monocytes. It is also detected in tumor margins (Panel 2D) that often contain activated LAK, monocytes, and macrophages. Therefore, antibody or small molecule antagonist therapies directed against the protein encoded by this transcript could reduce or inhibit inflammation in diseases such as asthma, emphysema, allergy, psoriasis, diabetes and arthritis. These treatments may also reduce or prevent tissue rejection after organ transplant. Agonistic therapies in contrast, my up regulate the function of LAK cells and aid in cancer treatments.

Panel 4D Summary: Ag1985 Expression of the CG96412-01 gene is in reasonable agreement with the results in Panel 4.1D. Highest expression of the gene is seen in LAK cells treated with PMA/ionomycin (CT=28.6). Please see Panel 4.1D for discussion of utility of this gene in inflammation.

N. CG96511-01: HsWECHE

Expression of gene CG96511-01 was assessed using the primer-probe sets Ag4063, Ag4171 and Ag4172, described in Tables NA, NB and NC. Results of the RTQ-PCR runs are shown in Tables ND and NE.

Table NA. Probe Name Ag4063

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttatgccgttatccagtgttgt-3'	22	963	182
Probe	TET-5'-tgtcccagcagcataacaaaggttaa-3'-TAMRA	26	986	183
Reverse	5'-gcaatcattgctgatgttgaat-3'	22	1022	184

Table NB. Probe Name Ag4171

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaagtggtctcaggggatttt-3'	21	415	185
Probe	TET-5'-ccaattccagctccatcaatttcctg-3'-TAMRA	26	446	186
Reverse	5'-gttgagtgacttggctgaagtc-3'	22	475	187

Table NC. Probe Name Ag4172

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gctctgtttccacaacctttc-3'	21	266	188
Probe	TET-5'-attctcttggcagagaacagtcccca-3'-TAMRA	26	290	189
Reverse	5'-actttggctcttgtatctgcat-3'	22	337	190

Table ND. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4063, Run 218905984	Tissue Name	Rel. Exp.(%) Ag4063, Run 218905984
Adipose	0.5	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	8.4
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	28.1
Melanoma* M14	0.0	Gastric ca. KATO III	**100.0**
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.6	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	2.7	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.3
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.3	Bone Marrow Pool	0.0
Ovary	0.2	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	8.5	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.3	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.9
Breast Pool	0.0	Thymus Pool	0.8
Trachea	1.3	CNS cancer	2.4

		(glio/astro) U87-MG	
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	5.8	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	1.1	CNS cancer (glio) SF-295	4.8
Lung ca. A549	11.3	Brain (Amygdala) Pool	0.5
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.4	Brain (fetal)	1.1
Lung ca. NCI-H460	63.3	Brain (Hippocampus) Pool	2.8
Lung ca. HOP-62	0.7	Cerebral Cortex Pool	1.3
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	3.6
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	3.5
Kidney Pool	0.7	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	4.0	Pancreas Pool	0.0

Table NE. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4063, Run 172572331	Tissue Name	Rel. Exp.(%) Ag4063, Run 172572331
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	7.6
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	3.5	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronery artery SMC rest	7.7
CD45RO CD4 lymphocyte act	0.0	Coronery artery SMC TNFalpha + IL-1beta	3.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	3.4

LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	13.3	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	17.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	6.5
Ramos (B cell) none	0.0	Lung fibroblast IL-13	7.9
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	6.7
EOL-1 dbcAMP	4.5	Dermal fibroblast CCD1070 IL-1 beta	4.1
EOL-1 dbcAMP PMA/ionomycin	3.1	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	3.8
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	42.0	Colon	0.0
Macrophages rest	1.7	Lung	0.0
Macrophages LPS	0.0	Thymus	14.7
HUVEC none	0.0	Kidney	**100.0**
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag4063/Ag4171/Ag4172 Results from these three experiment with the CG96511-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

General_screening_panel_v1.4 Summary: Ag4063 Highest expression of the CG96511-01 gene is detected in gastric cancer Kato III sample (CT=30.8). In addition,

significant expression of this gene is also detected in gastric (liver metastasis) cancer, lung cancer, renal cancer and breast cancer cell lines. Thus, expression of this gene can be used to distinguish between these samples and other samples in this panel. In addition, therapeutic modulation of the small chemokine encoded by this gene, through the use of

5   small molecule drugs, protein therapeutics or antibodies, might be beneficial in the treatment of these cancers.

Ag4171/Ag4172 Results from these two experiment with the CG96511-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

10   **Panel 4.1D Summary:** Ag4063 The CG96511-01 gene is only expressed at detectable levels in the kidney (CT=33.7). Therefore, espression of this gene could be used to distinguish the kidney sample from other samples used in this panel. In addition, antibody or small molecule therapies designed with the protein encoded for by this gene could modulate kidney function and be important in the treatment of inflammatory or

15   autoimmune diseases that affect the kidney, including lupus and glomerulonephritis.

Ag4171/Ag4172 Expression of the CG96511-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

O. CG96522-01: ADAM-TS 7 PRECURSOR

Expression of gene CG96522-01 was assessed using the primer-probe sets

20   Ag4084, Ag4322 and Ag4084, described in Tables OA, OB and OC.

Table OA. Probe Name Ag4084

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-atagaggacactggggttacca-3'	22	2581	191
Probe	TET-5'-atggttacctggtccccaaatcacct-3'-TAMRA	26	2607	192
Reverse	5'-gcttaggaattctggcacttg-3'	21	2641	193

Table OB. Probe Name Ag4322

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-catagaggacactggggttacc-3'	22	2580	194
Probe	TET-5'-atggttacctggtccccaaatcacct-3'-TAMRA	26	2607	195
Reverse	5'-gcttaggaattctggcacttg-3'	21	2641	196

Table OC. Probe Name Ag4084

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-atagaggacactggggttacca-3'	22	2581	197
Probe	TET-5'-atggttacctggtccccaaatcacct-3'-TAMRA	26	2607	198
Reverse	5'-gcttaggaattctggcacttg-3'	21	2641	199

CNS_neurodegeneration_v1.0 Summary: Ag4322 Expression of the CG96522-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Ag4084 Results from one experiment with the CG96522-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

General_screening_panel_v1.4 Summary: Ag4084/Ag4322 Expression of the CG96522-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag4084/Ag4322 Expression of the CG96522-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

P. CG96637-01: SMALL INDUCIBLE CYTOKINE A23 PRECURSOR

Expression of gene CG96637-01 was assessed using the primer-probe sets Ag4081 and Ag4345, described in Tables PA and PB. Results of the RTQ-PCR runs are shown in Tables PC and PD.

Table PA. Probe Name Ag4081

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gctgactgctgcatctccta-3'	20	162	200
Probe	TET-5'-acgaagcatcccgtgttcactcct-3'-TAMRA	24	188	201
Reverse	5'-tcgctgttcgtttcaaagtaac-3'	22	217	202

Table PB. Probe Name Ag4345

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgtcatgttcctcaccaaga-3'	21	253	203
Probe	TET-5'-acgtttctgtgccaaccccagtgata-3'-TAMRA	26	281	204
Reverse	5'-ctcacgcaaacctgaacttg-3'	20	309	205

Table PC. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4345, Run 224364194	Tissue Name	Rel. Exp.(%) Ag4345, Run 224364194
AD 1 Hippo	17.9	Control (Path) 3 Temporal Ctx	7.3
AD 2 Hippo	26.6	Control (Path) 4 Temporal Ctx	51.8
AD 3 Hippo	7.6	AD 1 Occipital Ctx	29.5
AD 4 Hippo	14.1	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	**100.0**	AD 3 Occipital Ctx	8.7
AD 6 Hippo	47.3	AD 4 Occipital Ctx	29.1
Control 2 Hippo	31.4	AD 5 Occipital Ctx	38.7
Control 4 Hippo	13.4	AD 6 Occipital Ctx	19.6
Control (Path) 3 Hippo	12.8	Control 1 Occipital Ctx	4.6
AD 1 Temporal Ctx	30.8	Control 2 Occipital Ctx	42.3
AD 2 Temporal Ctx	35.6	Control 3 Occipital Ctx	18.9
AD 3 Temporal Ctx	10.4	Control 4 Occipital Ctx	10.0
AD 4 Temporal Ctx	27.9	Control (Path) 1 Occipital Ctx	69.7
AD 5 Inf Temporal Ctx	71.7	Control (Path) 2 Occipital Ctx	17.9
AD 5 Sup Temporal Ctx	35.8	Control (Path) 3 Occipital Ctx	3.7
AD 6 Inf Temporal Ctx	49.3	Control (Path) 4 Occipital Ctx	22.2
AD 6 Sup Temporal Ctx	49.0	Control 1 Parietal Ctx	9.1
Control 1 Temporal Ctx	11.5	Control 2 Parietal Ctx	57.0
Control 2 Temporal Ctx	29.5	Control 3 Parietal Ctx	19.8
Control 3 Temporal Ctx	19.6	Control (Path) 1 Parietal Ctx	61.6
Control 3	12.4	Control (Path) 2	33.4

Temporal Ctx		Parietal Ctx	
Control (Path) 1 Temporal Ctx	48.6	Control (Path) 3 Parietal Ctx	5.2
Control (Path) 2 Temporal Ctx	48.0	Control (Path) 4 Parietal Ctx	45.7

Table PD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4345, Run 184565263	Rel. Exp.(%) Ag4345, Run 187509981	Tissue Name	Rel. Exp.(%) Ag4345, Run 184565263	Rel. Exp.(%) Ag4345, Run 187509981
Secondary Th1 act	0.0	0.0	HUVEC IL-1beta	0.9	0.0
Secondary Th2 act	0.4	0.0	HUVEC IFN gamma	5.4	14.1
Secondary Tr1 act	0.2	0.0	HUVEC TNF alpha + IFN gamma	0.2	1.2
Secondary Th1 rest	0.0	0.0	HUVEC TNF alpha + IL4	0.0	0.0
Secondary Th2 rest	0.7	0.6	HUVEC IL-11	2.6	3.8
Secondary Tr1 rest	0.3	0.0	Lung Microvascular EC none	0.3	0.4
Primary Th1 act	0.0	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0
Primary Th2 act	0.0	0.0	Microvascular Dermal EC none	0.0	0.0
Primary Tr1 act	0.0	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0
Primary Th1 rest	0.0	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0	0.0
Primary Th2 rest	0.0	0.0	Small airway epithelium none	0.0	0.0
Primary Tr1 rest	0.0	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	0.0	Coronery artery SMC rest	0.0	0.0
CD45RO CD4 lymphocyte act	0.0	0.0	Coronery artery SMC TNFalpha + IL-1beta	0.0	0.0

CD8 lymphocyte act	0.2	0.0	Astrocytes rest	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	Astrocytes TNFalpha + IL-1beta	0.0	0.0
Secondary CD8 lymphocyte act	0.3	0.0	KU-812 (Basophil) rest	0.3	0.9
CD4 lymphocyte none	0.0	0.7	KU-812 (Basophil) PMA/ionomycin	0.0	2.5
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	CCD1106 (Keratinocytes) none	0.0	0.0
LAK cells rest	1.0	2.4	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0
LAK cells IL-2	1.8	1.1	Liver cirrhosis	0.2	1.7
LAK cells IL-2+IL-12	0.0	0.0	NCI-H292 none	0.0	0.0
LAK cells IL-2+IFN gamma	0.4	0.7	NCI-H292 IL-4	0.0	0.0
LAK cells IL-2+ IL-18	0.3	0.0	NCI-H292 IL-9	0.0	0.0
LAK cells PMA/ionomycin	0.8	1.6	NCI-H292 IL-13	0.0	0.0
NK Cells IL-2 rest	1.2	3.1	NCI-H292 IFN gamma	0.0	0.0
Two Way MLR 3 day	1.5	5.7	HPAEC none	4.4	7.7
Two Way MLR 5 day	1.8	0.2	HPAEC TNF alpha + IL-1 beta	2.8	7.9
Two Way MLR 7 day	0.2	0.0	Lung fibroblast none	0.0	0.0
PBMC rest	0.0	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0	0.0
PBMC PWM	0.5	1.6	Lung fibroblast IL-4	0.0	0.0
PBMC PHA-L	3.5	7.5	Lung fibroblast IL-9	0.0	0.0
Ramos (B cell) none	0.9	0.0	Lung fibroblast IL-13	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	Lung fibroblast IFN gamma	0.0	0.0

B lymphocytes PWM	0.0	0.0	Dermal fibroblast CCD1070 rest	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.0	Dermal fibroblast CCD1070 TNF alpha	0.9	1.2
EOL-1 dbcAMP	5.6	12.1	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	1.7	0.0	Dermal fibroblast IFN gamma	0.0	0.0
Dendritic cells none	**100.0**	92.0	Dermal fibroblast IL-4	0.0	0.0
Dendritic cells LPS	24.3	50.3	Dermal Fibroblasts rest	0.0	0.0
Dendritic cells anti-CD40	15.6	30.6	Neutrophils TNFa+LPS	0.3	0.5
Monocytes rest	0.3	0.0	Neutrophils rest	3.8	7.0
Monocytes LPS	43.2	**100.0**	Colon	5.0	9.0
Macrophages rest	1.0	5.5	Lung	4.2	4.0
Macrophages LPS	15.0	14.0	Thymus	0.3	1.4
HUVEC none	0.0	0.4	Kidney	1.4	0.9
HUVEC starved	0.0	0.7			

CNS_neurodegeneration_v1.0 Summary: Ag4345 This panel confirms the expression of the CG96637-01 gene at low levels in the brains of an independent group of individuals. There is no differential expression of this gene between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. However, this gene may play a role in other central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Ag4081 Results from one experiment with the CG96637-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

General_screening_panel_v1.4 Summary: Ag4081 Expression of the CG96637-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag4345 Two experiments with same probe and primer sets are in excellent agreement with highest expression of the CG96637-01 gene in dentritic cells and LPS treated monocytes (CTs=29.4-30.6). In addition, expression of this

gene is stimulated in PHA-L treated PBMC cells, IFN gamma treated HUVEC, and LPS treated monocytes. Moderate expression of this gene is also detected in resting neutrophils, colon, lung, HPAEC, and dendritic cells. Therefore, therapeutic modulation of this gene product may be useful in the treatment of lupus erythematosus, asthma, emphysema, Crohn's disease, ulcerative colitis, rheumatoid arthritis, osteoarthritis, and psoriasis.

Ag4081 Expression of the CG96637-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Q. CG97274-01: GRANULOCYTE COLONY-STIMULATING FACTOR PRECURSOR

Expression of full length clone CG97274-01 was assessed using the primer-probe sets Ag4104 and Ag4120, described in Tables QA and QB. Results of the RTQ-PCR runs are shown in Tables QC, QD, QE, QF and QG.

Table QA. Probe Name Ag4104

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-agagcaagtgaggaagatcca-3'	21	116	206
Probe	TET-5'-caggctgcttgagccaactccatag-3'-TAMRA	25	169	207
Reverse	5'-cccctggtagaggaaaagg-3'	19	197	208

Table QB. Probe Name Ag4120

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-agctccctgccccagagctt-3'	20	81	209
Probe	TET-5'-tgctcaagtgcttagagcaagtgaggaaga-3'-TAMRA	30	103	210
Reverse	5'-gcagcctgccagcttctcc-3'	19	158	211

Table QC. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag4120, Run 211195146	Rel. Exp.(%) Ag4120, Run 215538807	Tissue Name	Rel. Exp.(%) Ag4120, Run 211195146	Rel. Exp.(%) Ag4120, Run 215538807
110967 COPD-F	0.0	7.6	112427 Match Control Psoriasis-F	0.0	0.0
110980 COPD-F	0.0	0.0	112418 Psoriasis-M	0.0	0.0
110968 COPD-M	0.0	0.0	112723 Match Control Psoriasis-M	0.0	0.0
110977 COPD-M	0.0	0.0	112419 Psoriasis-M	0.0	12.2
110989 Emphysema-F	0.0	2.0	112424 Match Control Psoriasis-M	0.0	0.0
110992 Emphysema-F	0.0	0.0	112420 Psoriasis-M	0.0	0.0
110993 Emphysema-F	0.0	9.5	112425 Match Control Psoriasis-M	0.0	0.0
110994 Emphysema-F	0.0	0.0	104689 (MF) OA Bone-Backus	0.0	0.0
110995 Emphysema-F	0.0	0.0	104690 (MF) Adj "Normal" Bone-Backus	0.0	0.0
110996 Emphysema-F	0.0	0.0	104691 (MF) OA Synovium-Backus	0.0	0.0
110997 Asthma-M	0.0	0.0	104692 (BA) OA Cartilage-Backus	0.0	0.0
111001 Asthma-F	0.0	0.0	104694 (BA) OA Bone-Backus	0.0	0.0
111002	0.0	0.0	104695 (BA)	0.0	0.0

Asthma-F			Adj "Normal" Bone-Backus		
111003 Atopic Asthma-F	0.0	0.0	104696 (BA) OA Synovium-Backus	0.0	0.0
111004 Atopic Asthma-F	0.0	42.3	104700 (SS) OA Bone-Backus	0.0	0.0
111005 Atopic Asthma-F	0.0	3.9	104701 (SS) Adj "Normal" Bone-Backus	0.0	0.0
111006 Atopic Asthma-F	0.0	0.0	104702 (SS) OA Synovium-Backus	0.0	0.0
111417 Allergy-M	0.0	2.5	117093 OA Cartilage Rep7	0.0	0.0
112347 Allergy-M	0.0	0.0	112672 OA Bone5	0.0	0.0
112349 Normal Lung-F	0.0	0.0	112673 OA Synovium5	0.0	0.0
112357 Normal Lung-F	0.0	0.0	112674 OA Synovial Fluid cells5	0.0	0.0
112354 Normal Lung-M	11.1	0.0	117100 OA Cartilage Rep14	0.0	0.0
112374 Crohns-F	0.0	0.0	112756 OA Bone9	0.0	0.0
112389 Match Control Crohns-F	0.0	0.0	112757 OA Synovium9	9.1	11.8
112375 Crohns-F	0.0	0.0	112758 OA Synovial Fluid Cells9	0.0	0.0
112732 Match Control Crohns-F	2.6	0.0	117125 RA Cartilage Rep2	2.3	4.1
112725 Crohns-M	0.0	0.0	113492 Bone2 RA	92.0	26.1
112387 Match Control	0.0	0.0	113493 Synovium2	49.3	48.0

Crohns-M			RA		
112378 Crohns-M	0.0	0.0	113494 Syn Fluid Cells RA	19.9	39.5
112390 Match Control Crohns-M	0.0	0.0	113499 Cartilage4 RA	34.4	34.6
112726 Crohns-M	14.8	11.9	113500 Bone4 RA	**100.0**	41.2
112731 Match Control Crohns-M	0.0	2.1	113501 Synovium4 RA	50.0	34.2
112380 Ulcer Col-F	0.0	0.0	113502 Syn Fluid Cells4 RA	26.8	42.9
112734 Match Control Ulcer Col-F	0.0	0.0	113495 Cartilage3 RA	41.5	26.4
112384 Ulcer Col-F	0.0	0.0	113496 Bone3 RA	48.0	38.7
112737 Match Control Ulcer Col-F	2.5	16.3	113497 Synovium3 RA	33.9	33.2
112386 Ulcer Col-F	0.0	0.0	113498 Syn Fluid Cells3 RA	85.9	**100.0**
112738 Match Control Ulcer Col-F	28.9	4.0	117106 Normal Cartilage Rep20	0.0	0.0
112381 Ulcer Col-M	4.6	0.0	113663 Bone3 Normal	0.0	0.0
112735 Match Control Ulcer Col-M	0.0	0.0	113664 Synovium3 Normal	0.0	0.0
112382 Ulcer Col-M	0.0	0.0	113665 Syn Fluid Cells3 Normal	0.0	0.0
112394 Match Control Ulcer Col-M	0.0	0.0	117107 Normal Cartilage Rep22	0.0	0.0
112383 Ulcer Col-M	0.0	0.0	113667 Bone4	0.0	0.0

			Normal		
112736 Match Control Ulcer Col-M	0.0	0.0	113668 Synovium4 Normal	0.0	0.0
112423 Psoriasis-F	28.9	10.6	113669 Syn Fluid Cells4 Normal	0.0	0.0

Table QD. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4120, Run 213323520	Rel. Exp.(%) Ag4120, Run 222181955	Tissue Name	Rel. Exp.(%) Ag4120, Run 213323520	Rel. Exp.(%) Ag4120, Run 222181955
Adipose	9.2	16.7	Renal ca. TK-10	0.0	0.0
Melanoma* Hs688(A).T	0.0	0.0	Bladder	0.3	0.0
Melanoma* Hs688(B).T	0.0	0.0	Gastric ca. (liver met.) NCI-N87	0.0	0.0
Melanoma* M14	0.0	0.0	Gastric ca. KATO III	0.0	0.0
Melanoma* LOXIMVI	31.9	35.4	Colon ca. SW-948	0.0	0.0
Melanoma* SK-MEL-5	0.0	0.0	Colon ca. SW480	0.0	0.0
Squamous cell carcinoma SCC-4	0.4	0.3	Colon ca.* (SW480 met) SW620	0.0	0.0
Testis Pool	0.0	0.0	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	0.0	0.6	Colon ca. HCT-116	0.0	0.0
Prostate Pool	0.0	0.0	Colon ca. CaCo-2	0.0	0.0
Placenta	0.0	0.0	Colon cancer tissue	1.1	0.4
Uterus Pool	0.0	0.0	Colon ca. SW1116	0.0	0.0
Ovarian ca. OVCAR-3	0.0	0.0	Colon ca. Colo-205	0.0	0.0
Ovarian ca. SK-OV-3	0.1	0.0	Colon ca. SW-48	0.0	0.0
Ovarian ca. OVCAR-4	0.0	0.0	Colon Pool	0.0	0.0
Ovarian ca. OVCAR-5	0.0	0.0	Small Intestine Pool	0.0	0.0
Ovarian ca. IGROV-1	0.0	0.0	Stomach Pool	0.8	0.0
Ovarian ca. OVCAR-8	0.0	0.0	Bone Marrow Pool	0.0	0.0
Ovary	0.0	0.0	Fetal Heart	0.0	0.0

Breast ca. MCF-7	0.0	0.0	Heart Pool	0.0	0.0
Breast ca. MDA-MB-231	0.0	0.0	Lymph Node Pool	0.0	0.0
Breast ca. BT 549	0.0	0.0	Fetal Skeletal Muscle	0.0	0.0
Breast ca. T47D	0.0	0.0	Skeletal Muscle Pool	1.4	0.5
Breast ca. MDA-N	0.0	0.0	Spleen Pool	0.0	0.0
Breast Pool	0.0	0.0	Thymus Pool	0.0	0.0
Trachea	0.7	1.3	CNS cancer (glio/astro) U87-MG	**100.0**	**100.0**
Lung	0.0	0.0	CNS cancer (glio/astro) U-118-MG	0.0	0.0
Fetal Lung	24.8	12.4	CNS cancer (neuro;met) SK-N-AS	0.0	0.0
Lung ca. NCI-N417	0.0	0.0	CNS cancer (astro) SF-539	0.0	0.0
Lung ca. LX-1	0.0	0.0	CNS cancer (astro) SNB-75	0.0	0.0
Lung ca. NCI-H146	0.0	0.0	CNS cancer (glio) SNB-19	0.0	0.0
Lung ca. SHP-77	0.0	0.9	CNS cancer (glio) SF-295	0.2	0.0
Lung ca. A549	0.1	0.0	Brain (Amygdala) Pool	0.2	0.6
Lung ca. NCI-H526	0.0	0.0	Brain (cerebellum)	0.2	0.3
Lung ca. NCI-H23	0.1	0.0	Brain (fetal)	0.3	0.0
Lung ca. NCI-H460	0.0	0.0	Brain (Hippocampus) Pool	0.8	1.1
Lung ca. HOP-62	0.0	0.0	Cerebral Cortex Pool	0.2	0.7
Lung ca. NCI-H522	0.0	0.0	Brain (Substantia nigra) Pool	1.1	0.0
Liver	0.0	0.0	Brain	0.9	0.4

			(Thalamus) Pool		
Fetal Liver	0.0	0.0	Brain (whole)	0.3	0.0
Liver ca. HepG2	0.0	0.0	Spinal Cord Pool	1.6	1.4
Kidney Pool	0.1	0.0	Adrenal Gland	0.7	0.0
Fetal Kidney	0.0	0.0	Pituitary gland Pool	0.2	0.0
Renal ca. 786-0	0.0	0.0	Salivary Gland	0.0	0.0
Renal ca. A498	0.0	0.0	Thyroid (female)	0.3	0.0
Renal ca. ACHN	0.0	0.0	Pancreatic ca. CAPAN2	0.0	0.0
Renal ca. UO-31	0.0	0.0	Pancreas Pool	0.0	0.0

Table QE. Panel 2.2

Tissue Name	Rel. Exp.(%) Ag4120, Run 173768884	Tissue Name	Rel. Exp.(%) Ag4120, Run 173768884
Normal Colon	0.0	Kidney Margin (OD04348)	0.0
Colon cancer (OD06064)	5.5	Kidney malignant cancer (OD06204B)	0.0
Colon Margin (OD06064)	0.0	Kidney normal adjacent tissue (OD06204E)	0.0
Colon cancer (OD06159)	0.0	Kidney Cancer (OD04450-01)	0.0
Colon Margin (OD06159)	0.0	Kidney Margin (OD04450-03)	0.0
Colon cancer (OD06297-04)	0.0	Kidney Cancer 8120613	0.0
Colon Margin (OD06297-05)	0.0	Kidney Margin 8120614	0.0
CC Gr.2 ascend colon (ODO3921)	0.0	Kidney Cancer 9010320	0.0
CC Margin (ODO3921)	5.9	Kidney Margin 9010321	0.0
Colon cancer metastasis (OD06104)	0.0	Kidney Cancer 8120607	0.0
Lung Margin (OD06104)	0.0	Kidney Margin 8120608	0.0
Colon mets to lung (OD04451-01)	0.0	Normal Uterus	0.0
Lung Margin (OD04451-02)	40.3	Uterine Cancer 064011	9.5
Normal Prostate	0.0	Normal Thyroid	0.0
Prostate Cancer (OD04410)	0.0	Thyroid Cancer 064010	0.0
Prostate Margin (OD04410)	0.0	Thyroid Cancer A302152	0.0
Normal Ovary	0.0	Thyroid Margin A302153	0.0
Ovarian cancer (OD06283-03)	0.0	Normal Breast	0.0
Ovarian Margin (OD06283-07)	0.0	Breast Cancer (OD04566)	0.0
Ovarian Cancer 064008	0.0	Breast Cancer 1024	0.0

Ovarian cancer (OD06145)	0.0	Breast Cancer (OD04590-01)	0.0
Ovarian Margin (OD06145)	0.0	Breast Cancer Mets (OD04590-03)	0.0
Ovarian cancer (OD06455-03)	0.0	Breast Cancer Metastasis (OD04655-05)	11.0
Ovarian Margin (OD06455-07)	23.8	Breast Cancer 064006	0.0
Normal Lung	5.8	Breast Cancer 9100266	0.0
Invasive poor diff. lung adeno (ODO4945-01	0.0	Breast Margin 9100265	0.0
Lung Margin (ODO4945-03)	**100.0**	Breast Cancer A209073	0.0
Lung Malignant Cancer (OD03126)	0.0	Breast Margin A2090734	0.0
Lung Margin (OD03126)	93.3	Breast cancer (OD06083)	0.0
Lung Cancer (OD05014A)	0.0	Breast cancer node metastasis (OD06083)	0.0
Lung Margin (OD05014B)	5.0	Normal Liver	0.0
Lung cancer (OD06081)	0.0	Liver Cancer 1026	5.4
Lung Margin (OD06081)	0.0	Liver Cancer 1025	0.0
Lung Cancer (OD04237-01)	0.0	Liver Cancer 6004-T	0.0
Lung Margin (OD04237-02)	77.4	Liver Tissue 6004-N	0.0
Ocular Melanoma Metastasis	0.0	Liver Cancer 6005-T	5.8
Ocular Melanoma Margin (Liver)	0.0	Liver Tissue 6005-N	0.0
Melanoma Metastasis	0.0	Liver Cancer 064003	0.0
Melanoma Margin (Lung)	4.5	Normal Bladder	0.0
Normal Kidney	0.0	Bladder Cancer 1023	0.0
Kidney Ca, Nuclear grade 2 (OD04338)	3.6	Bladder Cancer A302173	6.4
Kidney Margin (OD04338)	0.0	Normal Stomach	6.8

Kidney Ca Nuclear grade 1/2 (OD04339)	0.0	Gastric Cancer 9060397	0.0
Kidney Margin (OD04339)	0.0	Stomach Margin 9060396	0.0
Kidney Ca, Clear cell type (OD04340)	0.0	Gastric Cancer 9060395	3.7
Kidney Margin (OD04340)	0.0	Stomach Margin 9060394	1.8
Kidney Ca, Nuclear grade 3 (OD04348)	0.0	Gastric Cancer 064005	5.8

Table QF. Panel 3D

Tissue Name	Rel. Exp.(%) Ag4120, Run 184565476	Tissue Name	Rel. Exp.(%) Ag4120, Run 184565476
Daoy- Medulloblastoma	0.0	Ca Ski- Cervical epidermoid carcinoma (metastasis)	0.0
TE671- Medulloblastoma	0.0	ES-2- Ovarian clear cell carcinoma	0.0
D283 Med- Medulloblastoma	0.0	Ramos- Stimulated with PMA/ionomycin 6h	0.0
PFSK-1- Primitive Neuroectodermal	0.0	Ramos- Stimulated with PMA/ionomycin 14h	0.0
XF-498- CNS	0.0	MEG-01- Chronic myelogenous leukemia (megokaryoblast)	0.0
SNB-78- Glioma	0.0	Raji- Burkitt's lymphoma	0.0
SF-268- Glioblastoma	0.0	Daudi- Burkitt's lymphoma	0.0
T98G- Glioblastoma	0.0	U266- B-cell plasmacytoma	0.0
SK-N-SH- Neuroblastoma (metastasis)	0.0	CA46- Burkitt's lymphoma	0.0
SF-295- Glioblastoma	0.0	RL- non-Hodgkin's B-cell lymphoma	0.0
Cerebellum	0.0	JM1- pre-B-cell lymphoma	0.0
Cerebellum	0.0	Jurkat- T cell leukemia	0.0
NCI-H292- Mucoepidermoid lung carcinoma	0.0	TF-1- Erythroleukemia	0.0
DMS-114- Small cell lung cancer	0.0	HUT 78- T-cell lymphoma	0.0
DMS-79- Small cell lung cancer	0.0	U937- Histiocytic lymphoma	0.0
NCI-H146- Small cell lung cancer	0.0	KU-812- Myelogenous leukemia	0.0
NCI-H526- Small cell lung cancer	0.0	769-P- Clear cell renal carcinoma	0.0
NCI-N417- Small cell lung cancer	0.0	Caki-2- Clear cell renal carcinoma	0.0
NCI-H82- Small cell lung cancer	0.0	SW 839- Clear cell renal carcinoma	0.0
NCI-H157- Squamous cell lung cancer (metastasis)	0.0	G401- Wilms' tumor	0.0

NCI-H1155- Large cell lung cancer	0.0	Hs766T- Pancreatic carcinoma (LN metastasis)	0.0
NCI-H1299- Large cell lung cancer	0.0	CAPAN-1- Pancreatic adenocarcinoma (liver metastasis)	0.0
NCI-H727- Lung carcinoid	0.0	SU86.86- Pancreatic carcinoma (liver metastasis)	0.0
NCI-UMC-11- Lung carcinoid	0.0	BxPC-3- Pancreatic adenocarcinoma	0.0
LX-1- Small cell lung cancer	0.0	HPAC- Pancreatic adenocarcinoma	0.0
Colo-205- Colon cancer	0.0	MIA PaCa-2- Pancreatic carcinoma	0.0
KM12- Colon cancer	0.0	CFPAC-1- Pancreatic ductal adenocarcinoma	0.0
KM20L2- Colon cancer	0.0	PANC-1- Pancreatic epithelioid ductal carcinoma	0.0
NCI-H716- Colon cancer	0.0	T24- Bladder carcinma (transitional cell)	0.0
SW-48- Colon adenocarcinoma	0.0	5637- Bladder carcinoma	**100.0**
SW1116- Colon adenocarcinoma	0.0	HT-1197- Bladder carcinoma	0.0
LS 174T- Colon adenocarcinoma	0.0	UM-UC-3- Bladder carcinma (transitional cell)	0.0
SW-948- Colon adenocarcinoma	0.0	A204- Rhabdomyosarcoma	0.0
SW-480- Colon adenocarcinoma	0.0	HT-1080- Fibrosarcoma	0.0
NCI-SNU-5- Gastric carcinoma	0.0	MG-63- Osteosarcoma	0.0
KATO III- Gastric carcinoma	0.0	SK-LMS-1- Leiomyosarcoma (vulva)	0.0
NCI-SNU-16- Gastric carcinoma	0.0	SJRH30- Rhabdomyosarcoma (met to bone marrow)	0.0
NCI-SNU-1- Gastric carcinoma	0.0	A431- Epidermoid carcinoma	0.0
RF-1- Gastric adenocarcinoma	0.0	WM266-4- Melanoma	0.0
RF-48- Gastric adenocarcinoma	0.0	DU 145- Prostate carcinoma (brain metastasis)	0.0

MKN-45- Gastric carcinoma	0.0	MDA-MB-468- Breast adenocarcinoma	0.0
NCI-N87- Gastric carcinoma	0.0	SCC-4- Squamous cell carcinoma of tongue	0.0
OVCAR-5- Ovarian carcinoma	0.0	SCC-9- Squamous cell carcinoma of tongue	0.0
RL95-2- Uterine carcinoma	0.0	SCC-15- Squamous cell carcinoma of tongue	0.0
HelaS3- Cervical adenocarcinoma	0.0	CAL 27- Squamous cell carcinoma of tongue	0.0

Table QG. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4104, Run 172384092	Rel. Exp.(%) Ag4120, Run 172792551	Rel. Exp.(%) Ag4120, Run 173064519	Tissue Name	Rel. Exp.(%) Ag4104, Run 172384092	Rel. Exp.(%) Ag4120, Run 172792551	Rel. Exp.(%) Ag4120, Run 173064519
Secondary Th1 act	0.0	0.0	0.0	HUVEC IL-1beta	26.4	67.4	23.5
Secondary Th2 act	0.0	0.0	0.0	HUVEC IFN gamma	0.6	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	HUVEC TNF alpha + IFN gamma	0.0	2.0	0.0
Secondary Th1 rest	0.0	0.0	0.0	HUVEC TNF alpha + IL4	0.5	1.1	0.0
Secondary Th2 rest	0.0	0.0	0.0	HUVEC IL-11	0.0	0.0	0.0
Secondary Tr1 rest	0.0	0.0	0.0	Lung Microvascular EC none	0.5	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	Lung Microvascular EC TNFalpha + IL-1beta	29.7	15.1	7.1
Primary Th2 act	0.0	0.0	0.0	Microvascular Dermal EC none	2.4	1.2	0.0
Primary Tr1 act	0.0	0.0	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	29.3	26.8	5.6
Primary Th1 rest	0.0	0.0	0.0	Bronchial epithelium TNFalpha + IL1beta	3.0	2.2	0.0
Primary Th2 rest	0.0	0.0	0.0	Small airway epithelium none	1.9	0.0	0.0
Primary Tr1 rest	0.0	0.0	0.0	Small airway epithelium TNFalpha + IL-1beta	7.4	4.8	0.0
CD45RA CD4 lymphocyte	0.1	0.0	0.0	Coronery artery SMC rest	33.0	29.3	6.6

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CD45RO CD4 lymphocyte act	0.0	0.0	0.0	Coronery artery SMC TNFalpha + IL-1beta	**100.0**	40.6	81.8
CD8 lymphocyte act	0.0	0.0	0.0	Astrocytes rest	0.1	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	0.0	Astrocytes TNFalpha + IL-1beta	1.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	0.0	KU-812 (Basophil) rest	0.3	0.0	0.0
CD4 lymphocyte none	0.0	0.0	0.0	KU-812 (Basophil) PMA/iono mycin	0.0	0.0	0.0
2ry Th1/Th2/Tr 1_anti-CD95 CH11	0.0	0.0	0.0	CCD1106 (Keratinoc ytes) none	3.0	2.1	0.0
LAK cells rest	0.0	0.0	0.0	CCD1106 (Keratinoc ytes) TNFalpha + IL-1beta	1.5	3.8	4.6
LAK cells IL-2	0.0	0.0	0.0	Liver cirrhosis	0.0	0.0	1.5
LAK cells IL-2+IL-12	0.0	0.0	0.0	NCI-H292 none	0.0	1.5	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0	NCI-H292 IL-4	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	NCI-H292 IL-9	0.2	0.6	0.0
LAK cells PMA/ionom ycin	0.0	0.0	0.0	NCI-H292 IL-13	1.5	1.7	3.4
NK Cells IL-2 rest	0.0	0.0	0.0	NCI-H292 IFN gamma	0.0	1.9	0.0
Two Way MLR 3 day	0.0	0.0	0.0	HPAEC none	0.4	6.7	1.9
Two Way MLR 5 day	0.0	0.0	0.0	HPAEC TNF alpha + IL-1 beta	82.9	100.0	71.2
Two Way MLR 7 day	0.0	0.0	0.0	Lung fibroblast none	0.0	1.4	0.0
PBMC rest	0.0	0.0	0.0	Lung	44.1	35.4	14.4

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				fibroblast TNF alpha + IL-1 beta			
PBMC PWM	2.1	5.5	0.0	Lung fibroblast IL-4	0.0	0.0	0.0
PBMC PHA-L	0.3	1.2	0.0	Lung fibroblast IL-9	0.0	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0	Lung fibroblast IL-13	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	Lung fibroblast IFN gamma	0.0	0.0	0.0
B lymphocytes PWM	0.0	0.0	0.0	Dermal fibroblast CCD1070 rest	0.0	1.2	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	Dermal fibroblast CCD1070 TNF alpha	0.2	2.4	0.0
EOL-1 dbcAMP	0.0	0.0	0.0	Dermal fibroblast CCD1070 IL-1 beta	99.3	51.4	**100.0**
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	0.0	Dermal fibroblast IFN gamma	0.5	2.6	5.5
Dendritic cells none	0.0	0.0	0.0	Dermal fibroblast IL-4	0.0	0.4	2.4
Dendritic cells LPS	0.0	0.0	0.0	Dermal Fibroblasts rest	0.0	0.0	0.0
Dendritic cells anti-CD40	0.0	0.0	0.0	Neutrophils TNFa+LPS	1.2	4.5	2.6
Monocytes rest	0.0	0.0	0.0	Neutrophils rest	0.1	0.0	0.0
Monocytes LPS	54.3	35.4	39.2	Colon	0.0	2.0	0.0
Macrophages rest	0.0	0.0	0.0	Lung	0.4	0.0	1.3
Macrophages LPS	6.0	3.8	2.4	Thymus	0.0	2.3	0.0
HUVEC none	0.6	0.0	0.0	Kidney	0.0	7.5	1.6
HUVEC starved	0.9	0.0	0.0				

AI_comprehensive panel_v1.0 Summary: Ag4120 Two experiments with the same probe and primer show results that are in excellent agreement. Highest expression of the CG97274-01 is seen in samples derived from synovium of RA patients (CTs=33.4-33.5). In contrast, transcripts of variant CG97274-04 are produced at lower levels and in fewer tissue samples from RA patients. This shows disease tissue specific expression of this gene variant and distinguishes the expression pattern of CG97274-01 and CG97274-04. Results from a third experiment swith the same probe and primer show low/undetectable levels of expression (CTs>35) and are not included.

CNS_neurodegeneration_v1.0 Summary: Ag4120 Expression of the CG97274-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.) A third experiment with the probe and primer set Ag4104 is not included. The amp plot indicates that there were experimental difficulties with this run.

General_screening_panel_v1.4 Summary: Ag4120 Two experiments with the same probe and primer produce results that are in excellent agreement. Highest expression of the CG97274-01 gene is seen in a brain cancer cell line (CT=29-31.6) with significant expression also seen in a melanoma cell line. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of brain and melanoma cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of these cancers.

This gene is also expressed at moderate to low levels in adipose and fetal lung. In comparison, CG97274-04 is expressed at significant levels only in the cancer cell lines.

Panel 2.2 Summary: Ag4120 Expression of the CG97274-01 gene is restricted to samples derived from normal lung tissue (CTs=34). Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker of lung tissue. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of lung cancer.

Panel 3D Summary: Ag4120 Expression of the CG97274-01 gene is restricted to a sample derived from a bladder cancer cell line (CT=33.2). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker to detect the presence of bladder cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of bladder cancer.

Panel 4.1D Summary: Ag4120 Three experiments with the same probe and
primer set produce results that are in very good agreement. Highest expression of the
CG97274-01 gene is seen in TNF-alpha and IL-1 beta treated coronary artery SMCs and
HPAECs (CTs=29.4-31.7) and IL-1 beta treated dermal fibroblasts (CT=33). The
5   transcript is also induced in microvascular dermal endothelial cells, and lung
microvascular endothelial cells and LPS treated monocytes. Antibody therapeutics
designed against the protein encoded by the CG97274-01 gene may reduce or inhibit
inflammation or the tissue damage that results from inflammatory processes by blocking
the function of this protein, a putative member of the granulocytes colony stimulating
10   factor family. Members of this family have been shown to promote survival, proliferation
and terminal differentiation of granulocyte precursors (Metcalf, D. Science 229: 16-22,
1985. Souza LM, Science 1986 Apr 4;232(4746):61-5). Treatment with G-CSF protein
also induces allergic reactions (Sullivan AK, Int J STD AIDS 1997 Feb;8(2):135-6. Glass
LF, J Am Acad Dermatol 1996 Mar;34(3):455-9). Thus, the CG97274-01 gene product
15   may have similar functions as G-CSF in hematopoiesis and distinct functions in
autoimmune disorders such as rheumatoid arthritis. Based on the expression profile of the
CG97274-01 gene and on the known function of G-CSF, blocking the biological activity
of this protein with antibody therapeutics may reduce granulocyte participation in
diseases, particularly rheumatoid arthritis (based on expression in the A/I panel) and in
20   asthma, emphysema, allergy and other inflammatory conditions (based on panel 4.1). In
addition, protein therapeutics could also be designed with the protein encoded for by
CG97274-01. The protein could be inhibitory and block G-CSF interactions with the G-
CSF receptor and serve as an antagonistic protein therapeutic to block the specific
functions of G-CSF. The protein encoded by the CG97274-01 gene could also serve as an
25   agonistic protein therapeutic if it utilizes the GCSF receptor and functions similarly to
clinically utilized forms of G-CSF. Thus, it may play an important role in restoring
myelopoiesis after immunomodulatory treatments such as chemotherapy for cancer and
bone marrow transplant or in stimulating myelopoiesis in neutropenic disorders (Weaver
C, Bone Marrow Transplant 2001 May;27 Suppl 2:S23-9 Dale DC, Stem Cells 1995
30   Mar;13(2):94-100). Alternatively, based on expression in Panel 1.4 this gene product may
have a unique receptor and have agonistic protein therapeutic functions distinct from
CG97274-04, such as promoting lung development.

Panel 5D Summary: Ag4120 Expression of the CG97274-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

Panel CNS_1 Summary: Ag4120 Expression of the CG97274-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

5 **R. CG97274-04: Granulocyte colony-stimulating factor precursor (G-CSF3)**

Expression of gene CG97274-04 was assessed using the primer-probe set Ag4124, described in Table RA. Results of the RTQ-PCR runs are shown in Tables RB, RC and RD.

10   Table RA. Probe Name Ag4124

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-agctggtgagtgagtgtgcc-3'	20	371	212
Probe	TET-5'-tgccaccccgaggagctg-3'-TAMRA	18	403	213
Reverse	5'-atgcccagagagtgtccgag-3'	20	427	214

Table RB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4124, Run 212717374	Tissue Name	Rel. Exp.(%) Ag4124, Run 212717374
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	25.7	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.3	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	1.7
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.3
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.7
Breast ca. MDA-N	0.0	Spleen Pool	0.2
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.8	CNS cancer	**100.0**

		(glio/astro) U87-MG	
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.2
Fetal Lung	1.2	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.2
Lung ca. NCI-H23	0.0	Brain (fetal)	0.2
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.4
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.6
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.7
Liver	0.0	Brain (Thalamus) Pool	0.2
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.3
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Table RC. Panel 3D

Tissue Name	Rel. Exp.(%) Ag4124, Run 190820030	Tissue Name	Rel. Exp.(%) Ag4124, Run 190820030
Daoy- Medulloblastoma	0.0	Ca Ski- Cervical epidermoid carcinoma (metastasis)	0.0
TE671- Medulloblastoma	0.0	ES-2- Ovarian clear cell carcinoma	0.0
D283 Med- Medulloblastoma	0.0	Ramos- Stimulated with PMA/ionomycin 6h	0.0
PFSK-1- Primitive Neuroectodermal	0.0	Ramos- Stimulated with PMA/ionomycin 14h	0.0
XF-498- CNS	0.0	MEG-01- Chronic myelogenous leukemia (megokaryoblast)	0.0
SNB-78- Glioma	0.0	Raji- Burkitt's lymphoma	0.0
SF-268- Glioblastoma	0.0	Daudi- Burkitt's lymphoma	0.0
T98G- Glioblastoma	0.0	U266- B-cell plasmacytoma	0.0
SK-N-SH- Neuroblastoma (metastasis)	0.0	CA46- Burkitt's lymphoma	0.0
SF-295- Glioblastoma	0.0	RL- non-Hodgkin's B-cell lymphoma	0.0
Cerebellum	0.0	JM1- pre-B-cell lymphoma	0.0
Cerebellum	0.0	Jurkat- T cell leukemia	0.0
NCI-H292- Mucoepidermoid lung carcinoma	0.0	TF-1- Erythroleukemia	0.0
DMS-114- Small cell lung cancer	0.0	HUT 78- T-cell lymphoma	0.0
DMS-79- Small cell lung cancer	0.0	U937- Histiocytic lymphoma	0.0
NCI-H146- Small cell lung cancer	0.0	KU-812- Myelogenous leukemia	0.0
NCI-H526- Small cell lung cancer	0.0	769-P- Clear cell renal carcinoma	0.0
NCI-N417- Small cell lung cancer	0.0	Caki-2- Clear cell renal carcinoma	0.0
NCI-H82- Small cell lung cancer	0.0	SW 839- Clear cell renal carcinoma	0.0
NCI-H157- Squamous cell lung cancer (metastasis)	0.0	G401- Wilms' tumor	0.0

NCI-H1155- Large cell lung cancer	0.0	Hs766T- Pancreatic carcinoma (LN metastasis)	2.2
NCI-H1299- Large cell lung cancer	0.0	CAPAN-1- Pancreatic adenocarcinoma (liver metastasis)	0.0
NCI-H727- Lung carcinoid	0.0	SU86.86- Pancreatic carcinoma (liver metastasis)	6.2
NCI-UMC-11- Lung carcinoid	0.0	BxPC-3- Pancreatic adenocarcinoma	0.0
LX-1- Small cell lung cancer	0.0	HPAC- Pancreatic adenocarcinoma	0.0
Colo-205- Colon cancer	0.0	MIA PaCa-2- Pancreatic carcinoma	0.0
KM12- Colon cancer	0.0	CFPAC-1- Pancreatic ductal adenocarcinoma	0.0
KM20L2- Colon cancer	0.0	PANC-1- Pancreatic epithelioid ductal carcinoma	0.0
NCI-H716- Colon cancer	0.0	T24- Bladder carcinma (transitional cell)	6.7
SW-48- Colon adenocarcinoma	0.0	5637- Bladder carcinoma	**100.0**
SW1116- Colon adenocarcinoma	0.0	HT-1197- Bladder carcinoma	0.0
LS 174T- Colon adenocarcinoma	0.0	UM-UC-3- Bladder carcinma (transitional cell)	0.0
SW-948- Colon adenocarcinoma	0.0	A204- Rhabdomyosarcoma	0.0
SW-480- Colon adenocarcinoma	0.0	HT-1080- Fibrosarcoma	0.0
NCI-SNU-5- Gastric carcinoma	0.0	MG-63- Osteosarcoma	0.0
KATO III- Gastric carcinoma	9.7	SK-LMS-1- Leiomyosarcoma (vulva)	0.0
NCI-SNU-16- Gastric carcinoma	0.0	SJRH30- Rhabdomyosarcoma (met to bone marrow)	0.0
NCI-SNU-1- Gastric carcinoma	0.0	A431- Epidermoid carcinoma	0.0
RF-1- Gastric adenocarcinoma	0.0	WM266-4- Melanoma	0.0
RF-48- Gastric adenocarcinoma	0.0	DU 145- Prostate carcinoma (brain metastasis)	0.0

MKN-45- Gastric carcinoma	3.0	MDA-MB-468- Breast adenocarcinoma	0.0
NCI-N87- Gastric carcinoma	0.0	SCC-4- Squamous cell carcinoma of tongue	0.0
OVCAR-5- Ovarian carcinoma	0.0	SCC-9- Squamous cell carcinoma of tongue	0.0
RL95-2- Uterine carcinoma	0.0	SCC-15- Squamous cell carcinoma of tongue	0.0
HelaS3- Cervical adenocarcinoma	0.0	CAL 27- Squamous cell carcinoma of tongue	0.0

Table RD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4124, Run 172859313	Tissue Name	Rel. Exp.(%) Ag4124, Run 172859313
Secondary Th1 act	0.0	HUVEC IL-1beta	16.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.9
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.3
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.4
Secondary Th2 rest	0.0	HUVEC IL-11	0.1
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	14.1
Primary Th2 act	0.0	Microvascular Dermal EC none	0.3
Primary Tr1 act	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	10.8
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	2.6
Primary Th2 rest	0.0	Small airway epithelium none	2.7
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	3.6
CD45RA CD4 lymphocyte act	0.0	Coronery artery SMC rest	18.2
CD45RO CD4 lymphocyte act	0.0	Coronery artery SMC TNFalpha + IL-1beta	48.3
CD8 lymphocyte act	0.0	Astrocytes rest	0.5
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.9
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.6
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	2.9
LAK cells IL-2	0.0	Liver cirrhosis	0.0

LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.1
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.5
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	1.4
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	**100.0**
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	30.4
PBMC PWM	1.2	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.6	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	48.6
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	14.7	Colon	0.0
Macrophages rest	0.0	Lung	0.4
Macrophages LPS	2.6	Thymus	0.0
HUVEC none	0.0	Kidney	0.1
HUVEC starved	0.0		

AI_comprehensive panel_v1.0 Summary: Ag4124 Expression of the CG97274-04 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.) Please note that this lack of detectable expression is in contrast with the expression profile of the CG97274-01 variant.

CNS_neurodegeneration_v1.0 Summary: Ag4124 Expression of the CG97274-04 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag4124 Expression of the CG97274-04 gene is restricted to samples derived from a brain cancer and a melanoma cell line

5 (CTs=30-32). Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of brain and melanoma cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of these cancers.

Panel 3D Summary: Ag4124 Expression of the CG97274-04 gene is restricted to

10 a sample derived from a bladder cancer cell line (CT=33). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker to detect the presence of bladder cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of bladder cancer.

Panel 4.1D Summary: Ag4124 Expression of the CG97274-04 gene is highest in

15 TNF-alpha and IL-1 beta HPAEC cells (CT=29.4). In addition, expression is seen in other TNF-alpha and/or IL-1 beta treated samples including dermal fibroblasts, lung fibroblasts, coronary artery SMCs, lung microvasculature, small airway epithelium and keratinocytes. Since expression of this transcript appears to be up regulated by the cytokine TNF-a, therapeutic modulation of the function or expression of the protein encoded by this gene

20 may reduce or eliminate inflammation and tissue damage that result from diseases associated with hyperactivated T cells including lupus erythematosus, rheumatoid arthritis, and inflammatory bowel diseases.

Panel CNS_1 Summary: Ag4124 Expression of the CG97274-04 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

25 **general oncology screening panel_v_2.4 Summary:** Ag4124 Expression of the CG97274-04 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

S. CG97288-01 and CG97288-02: HsPLP2Long

Expression of gene CG97288-01 and variant CG97288-02 was assessed using the

30 primer-probe set Ag4173, described in Table SA. Results of the RTQ-PCR runs are shown in Tables SB, SC and SD.

Table SA. Probe Name Ag4173

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-atgagcctcagacttgatacca-3'	22	1	215
Probe	TET-5'-taacagtgcgagaccacttcatgcct-3'-TAMRA	26	33	216
Reverse	5'-agtcagcagcaatgacagaag-3'	21	73	217

Table SB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4173, Run 215539057	Tissue Name	Rel. Exp.(%) Ag4173, Run 215539057
AD 1 Hippo	10.5	Control (Path) 3 Temporal Ctx	12.2
AD 2 Hippo	5.2	Control (Path) 4 Temporal Ctx	7.0
AD 3 Hippo	13.3	AD 1 Occipital Ctx	7.9
AD 4 Hippo	1.8	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	28.9	AD 3 Occipital Ctx	13.6
AD 6 Hippo	27.9	AD 4 Occipital Ctx	6.6
Control 2 Hippo	0.0	AD 5 Occipital Ctx	2.2
Control 4 Hippo	11.7	AD 6 Occipital Ctx	**100.0**
Control (Path) 3 Hippo	13.4	Control 1 Occipital Ctx	8.9
AD 1 Temporal Ctx	5.2	Control 2 Occipital Ctx	0.8
AD 2 Temporal Ctx	9.5	Control 3 Occipital Ctx	4.3
AD 3 Temporal Ctx	4.2	Control 4 Occipital Ctx	8.0
AD 4 Temporal Ctx	5.8	Control (Path) 1 Occipital Ctx	4.2
AD 5 Inf Temporal Ctx	25.0	Control (Path) 2 Occipital Ctx	1.2
AD 5 Sup Temporal Ctx	55.9	Control (Path) 3 Occipital Ctx	6.9
AD 6 Inf Temporal Ctx	25.3	Control (Path) 4 Occipital Ctx	5.3
AD 6 Sup Temporal Ctx	30.6	Control 1 Parietal Ctx	3.6
Control 1 Temporal Ctx	9.0	Control 2 Parietal Ctx	22.8
Control 2 Temporal Ctx	2.0	Control 3 Parietal Ctx	5.1
Control 3 Temporal Ctx	2.4	Control (Path) 1 Parietal Ctx	3.3
Control 3	11.7	Control (Path) 2	8.2

Temporal Ctx		Parietal Ctx	
Control (Path) 1 Temporal Ctx	1.9	Control (Path) 3 Parietal Ctx	8.5
Control (Path) 2 Temporal Ctx	5.6	Control (Path) 4 Parietal Ctx	6.8

Table SC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4173, Run 219840030	Tissue Name	Rel. Exp.(%) Ag4173, Run 219840030
Adipose	6.7	Renal ca. TK-10	0.1
Melanoma* Hs688(A).T	0.0	Bladder	1.7
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.4
Melanoma* M14	0.0	Gastric ca. KATO III	0.5
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.5
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.1	Colon ca. HT29	0.1
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.2	Colon ca. CaCo-2	0.1
Placenta	3.8	Colon cancer tissue	24.1
Uterus Pool	0.2	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.3
Ovarian ca. OVCAR-5	6.2	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.3
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.1
Ovary	0.2	Fetal Heart	5.3
Breast ca. MCF-7	0.0	Heart Pool	0.3
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.1
Breast ca. BT 549	0.1	Fetal Skeletal Muscle	0.5
Breast ca. T47D	9.5	Skeletal Muscle Pool	0.2
Breast ca. MDA-N	0.1	Spleen Pool	22.1
Breast Pool	0.4	Thymus Pool	0.4
Trachea	0.3	CNS cancer	0.0

		(glio/astro) U87-MG	
Lung	0.4	CNS cancer (glio/astro) U-118-MG	0.1
Fetal Lung	37.9	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.1	Brain (Amygdala) Pool	0.1
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.3
Lung ca. NCI-H23	0.0	Brain (fetal)	0.4
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.2
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.2
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.4	Brain (Thalamus) Pool	0.1
Fetal Liver	**100.0**	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	0.2
Kidney Pool	0.4	Adrenal Gland	0.8
Fetal Kidney	4.2	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.2
Renal ca. A498	0.0	Thyroid (female)	3.5
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.2
Renal ca. UO-31	0.0	Pancreas Pool	0.2

Table SD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4173, Run 173507622	Tissue Name	Rel. Exp.(%) Ag4173, Run 173507622
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.1	HUVEC IFN gamma	0.1
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.1
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.1	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.1	Bronchial epithelium TNFalpha + IL1beta	0.8
Primary Th2 rest	0.1	Small airway epithelium none	0.1
Primary Tr1 rest	0.2	Small airway epithelium TNFalpha + IL-1beta	1.0
CD45RA CD4 lymphocyte act	0.0	Coronery artery SMC rest	0.1
CD45RO CD4 lymphocyte act	0.6	Coronery artery SMC TNFalpha + IL-1beta	0.1
CD8 lymphocyte act	0.1	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	2.9	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.3
CD4 lymphocyte none	11.6	KU-812 (Basophil) PMA/ionomycin	0.5
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	15.5	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.1
LAK cells IL-2	1.9	Liver cirrhosis	0.7

LAK cells IL-2+IL-12	0.9	NCI-H292 none	0.9
LAK cells IL-2+IFN gamma	2.0	NCI-H292 IL-4	0.5
LAK cells IL-2+ IL-18	1.5	NCI-H292 IL-9	0.5
LAK cells PMA/ionomycin	21.5	NCI-H292 IL-13	0.5
NK Cells IL-2 rest	1.4	NCI-H292 IFN gamma	1.4
Two Way MLR 3 day	4.4	HPAEC none	0.0
Two Way MLR 5 day	0.4	HPAEC TNF alpha + IL-1 beta	4.1
Two Way MLR 7 day	0.3	Lung fibroblast none	0.0
PBMC rest	70.7	Lung fibroblast TNF alpha + IL-1 beta	0.2
PBMC PWM	10.7	Lung fibroblast IL-4	0.0
PBMC PHA-L	15.1	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.2
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.2
EOL-1 dbcAMP PMA/ionomycin	13.7	Dermal fibroblast IFN gamma	0.8
Dendritic cells none	0.2	Dermal fibroblast IL-4	1.2
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.6
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	19.5
Monocytes rest	14.1	Neutrophils rest	14.4
Monocytes LPS	**100.0**	Colon	1.0
Macrophages rest	13.1	Lung	1.4
Macrophages LPS	7.8	Thymus	3.5
HUVEC none	0.0	Kidney	28.9
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag4173 This panel confirms the
expression of the CG97288-01 gene at low levels in the brains of an independent group of
individuals. However, no differential expression of this gene was detected between
Alzheimer's diseased postmortem brains and those of non-demented controls in this

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experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag4173 Highest expression of the CG97288-01 is detected in fetal liver (CT=26). Interestingly, this gene is expressed at

5   much higher levels in fetal when compared to adult liver(CT=34). This observation suggests that expression of this gene can be used to distinguish fetal from adult liver. In addition, the relative overexpression of this gene in fetal liver suggests that the protein product may enhance liver growth or development in the fetus and thus may also act in a regenerative capacity in the adult. Therefore, therapeutic modulation of the protein

10   encoded by this gene could be useful in treatment of liver related diseases.

Among tissues with metabolic or endocrine function, this gene is expressed at low to moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related

15   diseases, such as obesity and diabetes.

Low to moderate expression of this gene is also detected in colon cancer tissue, a breast cancer and an ovarian cancer cell lines. Therefore, therapeutic modulation of this gene product could be useful in the treatment of these cancers.

In addition, this gene is expressed at moderate levels in cerebellum, fetal and adult

20   whole brain. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Interestingly, this gene is expressed at much higher levels in fetal (CTs=27-30) when compared to adult heart, lung and kidney(CTs=34). This observation suggests that

25   expression of this gene can be used to distinguish these fetal from the corresponding adult tissue. In addition, the relative overexpression of this gene in fetal tissue suggests that the protein product may play a role in lung, heart and kidney development in the fetus and thus may also act in a regenerative capacity in the adult. Therefore, therapeutic modulation of the protein encoded by this gene could be useful in treatment of lung, heart and kidney

30   related diseases.

Panel 4.1D Summary: Ag4173 Highest expression of the CG97288-01 is detected in LPS treated monocytes (CT=28.5). Significant expression of this gene is thymus, PBMC cells, neutrophils, macrophages, LAK cells, CD4 and secondary CD8

lymphocytes. In addition, expression of this gene is stimulated in LPS treated monocytes, PMA/ionomycing treated EOL-1 dbcAMP, TNF alpha + IL-1 beta treated HPAEC cells. Therefore, therapeutic modulation of this gene product could be beneficial in the treatment of autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

In addition, moderate expression is also detected in kidney (CT=30). Therefore, antibody or small molecule therapies designed with the protein encoded for by this gene could modulate kidney function and be important in the treatment of inflammatory or autoimmune diseases that affect the kidney, including lupus and glomerulonephritis.

T. CG97550-01: Serine Protease

Expression of gene CG97550-01 was assessed using the primer-probe sets Ag1156, Ag1411 and Ag384, described in Tables TA, TB and TC. Results of the RTQ-PCR runs are shown in Tables TD, TE and TF.

Table TA. Probe Name Ag1156

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gaggtcagcagtggaatttatg-3'	22	1336	218
Probe	TET-5'-aattcaccttctcagagaggcggcat-3'-TAMRA	26	1375	219
Reverse	5'-cttgacgatgatgtcaccatct-3'	22	1404	220

Table TB. Probe Name Ag1411

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gaggtcagcagtggaatttatg-3'	22	1336	221
Probe	TET-5'-aattcaccttctcagagaggcggcat-3'-TAMRA	26	1375	222
Reverse	5'-cttgacgatgatgtcaccatct-3'	22	1404	223

Table TC. Probe Name Ag384

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gggagtttgtggtggccat-3'	19	953	224
Probe	TET-5'-tcccttcgccctacagaacacagtgaca-3'-TAMRA	28	978	225
Reverse	5'-tgggcagtgctgacgatg-3'	18	1011	226

Table TD. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag384, Run 225436660	Tissue Name	Rel. Exp.(%) Ag384, Run 225436660
AD 1 Hippo	19.9	Control (Path) 3 Temporal Ctx	24.0
AD 2 Hippo	50.7	Control (Path) 4 Temporal Ctx	38.2
AD 3 Hippo	18.3	AD 1 Occipital Ctx	8.8
AD 4 Hippo	23.3	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	52.9	AD 3 Occipital Ctx	28.3
AD 6 Hippo	**100.0**	AD 4 Occipital Ctx	7.7
Control 2 Hippo	20.2	AD 5 Occipital Ctx	39.5
Control 4 Hippo	44.1	AD 6 Occipital Ctx	33.4
Control (Path) 3 Hippo	40.9	Control 1 Occipital Ctx	53.6
AD 1 Temporal Ctx	27.2	Control 2 Occipital Ctx	68.8
AD 2 Temporal Ctx	37.6	Control 3 Occipital Ctx	16.3
AD 3 Temporal Ctx	10.4	Control 4 Occipital Ctx	6.4
AD 4 Temporal Ctx	12.7	Control (Path) 1 Occipital Ctx	45.7
AD 5 Inf Temporal Ctx	69.3	Control (Path) 2 Occipital Ctx	23.5
AD 5 SupTemporal Ctx	56.6	Control (Path) 3 Occipital Ctx	12.2
AD 6 Inf Temporal Ctx	53.2	Control (Path) 4 Occipital Ctx	44.8
AD 6 Sup Temporal Ctx	69.7	Control 1 Parietal Ctx	16.0
Control 1 Temporal Ctx	75.3	Control 2 Parietal Ctx	12.3
Control 2 Temporal Ctx	22.7	Control 3 Parietal Ctx	16.0
Control 3 Temporal Ctx	33.2	Control (Path) 1 Parietal Ctx	47.6
Control 4 Temporal	22.5	Control (Path) 2	52.1

Ctx		Parietal Ctx	
Control (Path) 1 Temporal Ctx	54.0	Control (Path) 3 Parietal Ctx	7.9
Control (Path) 2 Temporal Ctx	12.1	Control (Path) 4 Parietal Ctx	14.7

Table TE. Panel 1.1

Tissue Name	Rel. Exp.(%) Ag384, Run 111793768	Rel. Exp.(%) Ag384, Run 121147677	Tissue Name	Rel. Exp.(%) Ag384, Run 111793768	Rel. Exp.(%) Ag384, Run 121147677
Adrenal gland	2.1	1.3	Renal ca. UO-31	0.0	0.0
Bladder	21.6	16.6	Renal ca. RXF 393	0.0	0.0
Brain (amygdala)	0.0	0.0	Liver	0.2	0.1
Brain (cerebellum)	0.0	0.0	Liver (fetal)	0.0	0.1
Brain (hippocampus)	0.0	0.0	Liver ca. (hepatoblast) HepG2	0.0	0.0
Brain (substantia nigra)	0.0	0.0	Lung	7.5	6.1
Brain (thalamus)	0.0	0.0	Lung (fetal)	10.5	11.9
Cerebral Cortex	0.0	0.0	Lung ca. (non-s.cell) HOP-62	46.0	48.3
Brain (fetal)	0.0	0.0	Lung ca. (large cell)NCI-H460	0.0	0.0
Brain (whole)	0.0	0.0	Lung ca. (non-s.cell) NCI-H23	0.0	0.1
glio/astro U-118-MG	0.0	0.0	Lung ca. (non-s.cl) NCI-H522	0.0	0.0
astrocytoma SF-539	0.0	0.0	Lung ca. (non-sm. cell) A549	0.0	0.0
astrocytoma SNB-75	0.0	0.0	Lung ca. (s.cell var.) SHP-77	0.0	0.0
astrocytoma SW1783	0.0	0.0	Lung ca. (small cell) LX-1	0.0	0.0
glioma U251	0.0	0.0	Lung ca. (small cell)	0.0	0.0

			NCI-H69		
glioma SF-295	0.0	0.0	Lung ca. (squam.) SW 900	0.0	0.0
glioma SNB-19	0.0	0.0	Lung ca. (squam.) NCI-H596	0.0	0.0
glio/astro U87-MG	0.0	0.0	Lymph node	0.7	2.0
neuro*; met SK-N-AS	0.0	0.0	Spleen	0.0	0.0
Mammary gland	26.8	19.6	Thymus	0.1	0.1
Breast ca. BT-549	0.0	0.0	Ovary	60.3	70.7
Breast ca. MDA-N	0.0	0.0	Ovarian ca. IGROV-1	0.0	0.0
Breast ca.* (pl.ef) T47D	0.0	0.0	Ovarian ca. OVCAR-3	0.0	0.0
Breast ca.* (pl.ef) MCF-7	0.0	0.0	Ovarian ca. OVCAR-4	0.0	0.0
Breast ca.* (pl.ef) MDA-MB-231	1.0	0.8	Ovarian ca. OVCAR-5	0.0	0.1
Small intestine	20.0	20.0	Ovarian ca. OVCAR-8	0.0	0.0
Colorectal	0.0	0.1	Ovarian ca.* (ascites) SK-OV-3	0.0	0.0
Colon ca. HT29	0.0	0.0	Pancreas	11.8	8.9
Colon ca. CaCo-2	0.0	0.0	Pancreatic ca. CAPAN 2	0.0	0.0
Colon ca. HCT-15	0.0	0.0	Pituitary gland	0.3	1.1
Colon ca. HCT-116	0.0	0.0	Placenta	10.5	9.8
Colon ca. HCC-2998	0.0	0.0	Prostate	2.1	4.9
Colon ca. SW480	0.0	0.0	Prostate ca.* (bone met) PC-3	0.7	2.2
Colon ca.* SW620 (SW480 met)	0.0	0.0	Salivary gland	9.0	10.0

Stomach	17.3	20.6	Trachea	7.7	5.3
Gastric ca. (liver met) NCI-N87	0:0	0.0	Spinal cord	0.1	0.0
Heart	**100.0**	90.1	Testis	0.2	1.7
Skeletal muscle (Fetal)	29.5	24.3	Thyroid	16.3	7.6
Skeletal muscle	0.0	60.3	Uterus	17.0	10.1
Endothelial cells	0.6	4.7	Melanoma M14	0.0	0.0
Heart (Fetal)	62.4	**100.0**	Melanoma LOX IMVI	0.0	0.0
Kidney	0.6	2.5	Melanoma UACC-62	0.0	0.0
Kidney (fetal)	1.2	2.5	Melanoma SK-MEL-28	0.0	0.0
Renal ca. 786-0	0.0	0.0	Melanoma* (met) SK-MEL-5	0.0	0.0
Renal ca. A498	0.0	0.0	Melanoma Hs688(A).T	0.6	0.1
Renal ca. ACHN	0.0	0.0	Melanoma* (met) Hs688(B).T	0.0	0.0
Renal ca. TK-10	0.0	0.0			

Table TF. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag384, Run 182392292	Tissue Name	Rel. Exp.(%) Ag384, Run 182392292
Secondary Th1 act	0.0	HUVEC IL-1beta	23.5
Secondary Th2 act	0.0	HUVEC IFN gamma	18.4
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	8.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	9.2
Secondary Th2 rest	0.0	HUVEC IL-11	16.2
Secondary Tr1 rest	0.0	Lung Microvascular EC none	24.7
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	15.0
Primary Th2 act	0.0	Microvascular Dermal EC none	7.5
Primary Tr1 act	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	0.1
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	2.2
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	3.6	Coronery artery SMC rest	12.5
CD45RO CD4 lymphocyte act	0.0	Coronery artery SMC TNFalpha + IL-1beta	8.1
CD8 lymphocyte act	0.0	Astrocytes rest	0.7
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	11.1
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	4.2
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	7.6
LAK cells IL-2+IL-12	0.1	NCI-H292 none	0.0

LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.3
Two Way MLR 3 day	0.1	HPAEC none	24.1
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	20.4
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	1.3
PBMC PWM	0.0	Lung fibroblast IL-4	2.1
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.3
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	2.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	19.2
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	8.7
EOL-1 dbcAMP	0.1	Dermal fibroblast CCD1070 IL-1 beta	5.5
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	47.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	68.3
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	24.1
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	2.0
Monocytes rest	0.0	Neutrophils rest	0.6
Monocytes LPS	4.9	Colon	12.2
Macrophages rest	6.6	Lung	**100.0**
Macrophages LPS	0.0	Thymus	29.1
HUVEC none	31.0	Kidney	41.8
HUVEC starved	27.2		

CNS_neurodegeneration_v1.0 Summary: Ag384 This panel confirms the expression of the CG97550-01 gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Low levels of expression in the brain suggests that this gene may play a role

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in central nervous system disorders such as Parkinson's disease, epilepsy, multiple

sclerosis, schizophrenia and depression.

Panel 1.1 Summary: Ag384 Two experiments with excellent agreement with

highest expression of the CG97550-01 gene in heart (CTs=22). Expression of this gene is

5   seen exclusively in almost all the normal tissue samples used in this panel. This expression

in normal tissues suggests that this gene product may play an important role in cellular

function. Interestingly, high expression of this gene is also detected in a lung cancer (non-

small cell) HOP-62 cell line and prostate cancer bone metastasis cell line PC3. Thus,

expression of this gene can be used as a diagnostic marker for lung and prostate cancer.

10   Also, therapeutic modulation of the activity of this gene or its protein product, through the

use of small molecule drugs, protein therapeutics or antibodies, might be beneficial in the

treatment of lung cancer or prostate cancer.

Among tissues with metabolic or endocrine function, this gene is expressed at high

to moderate levels in pancreas, adrenal gland, thyroid, pituitary gland, skeletal muscle,

15   heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity

of this gene may prove useful in the treatment of endocrine/metabolically related diseases,

such as obesity and diabetes.

Panel 4.1D Summary: Ag384 Highest expression of the CG97550-01 gene is

detected in lung (CTs=30.15). Moderate expression of this gene is also seen in dermal

20   fibroblasts, HPAEC cells, coronery artery SMC cells, HUVEC cells, lung and dermal

microvascular EC cells and liver cirrhosis sample. In addition, expression of this gene is

stimulated in LPS treated monocytes, TNFalpha + IL-1beta treated astrocytes, and

PMA/ionomycin treated basophils. The CG97550-01 gene codes for a serine protease.

Proteins belonging to serine protease family have been implicated in numerous

25   inflammatory and malignant diseases wherein inflammatory cells such as

monocytes/macrophages are involved. Such diseases include lung cancer, chronic

inflammatory bowel disease, vasculitis and connective tissue disease, bacterial sepsis, and

septic shock (Heiden et al., 1996, Semin Thromb Hemost 22(6):497-501, PMID:

9122714). Therefore, therapeutic modulation of the serine protease encoded by this gene

30   could be beneficial in the treatement of asthma, allergies, inflammatory bowel disease,

lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Significant expression of this gene is also seen in normal colon, lung, thymus and

kidney tissue. This pattern is in agreement with the expression profile in

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General_screening_panel_v1.4 and also suggests a role for the gene product in cell survival and proliferation.

Therefore, therapeutic modulation of this gene product may be useful in treatment of inflammatory disease of these tissues.

5   **U. CG97800-01 and CG97800-02 and CG97800-03: Elastase IV-like**

Expression of gene CG97800-01 and full length clones CG97800-02 and CG97800-03 was assessed using the primer-probe set Ag4156, described in Table UA. Results of the RTQ-PCR runs are shown in Tables UB and UC. Please note that CG97800-03 represents a full-length physical clone of the CG97800-01 gene, validating

10   the prediction of the gene sequence.

Table UA. Probe Name Ag4156

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-acgtccacaagagatggaatg-3'	21	376	227
Probe	TET-5'-tgatattgccctcatcaagcttgcag-3'-TAMRA	26	413	228
Reverse	5'-gtcactcagctccacatgct-3'	20	439	229

Table UB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4156, Run 221034285	Tissue Name	Rel. Exp.(%) Ag4156, Run 221034285
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	**100.0**
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.1	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.1	CNS cancer	0.0

		(glio/astro) U87-MG	
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.1
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.1	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	1.3	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	60.3

Table UC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4156, Run 173123941	Tissue Name	Rel. Exp.(%) Ag4156, Run 173123941
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	6.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	32.1	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	5.4
Primary Th2 act	4.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	6.0	Microsvasular Dermal EC TNFalpha + IL-1beta	4.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	12.8	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronery artery SMC rest	0.0
CD45RO CD4 lymphocyte act	9.2	Coronery artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	6.7	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	7.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	8.4	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	3.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	3.3	Liver cirrhosis	6.6

LAK cells IL-2+IL-12	7.8	NCI-H292 none	6.6
LAK cells IL-2+IFN gamma	7.3	NCI-H292 IL-4	17.2
LAK cells IL-2+ IL-18	15.2	NCI-H292 IL-9	7.0
LAK cells PMA/ionomycin	**100.0**	NCI-H292 IL-13	8.9
NK Cells IL-2 rest	43.8	NCI-H292 IFN gamma	11.7
Two Way MLR 3 day	15.9	HPAEC none	4.5
Two Way MLR 5 day	7.7	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	8.0	Lung fibroblast none	6.7
PBMC rest	8.5	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	7.5
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	21.5
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	8.2
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	7.4	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	45.7	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	28.9	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	6.5	Neutrophils TNFa+LPS	68.3
Monocytes rest	7.1	Neutrophils rest	25.5
Monocytes LPS	68.3	Colon	0.0
Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	27.9
HUVEC none	0.0	Kidney	0.0
HUVEC starved	6.0		

CNS_neurodegeneration_v1.0 Summary: Ag4156 Expression of the CG97800-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag4156 Expression of the CG97800-01 gene, an elastase homolog, is limited to the pancreas and bladder (CTs=24.3-25.1).

5   Elastases are proteinases that dissolve elastin. They have been implicated in the pathology

of infections and inflammation. Based on the pattern of expression of this putative elastin, expression of this gene could be used as a marker of bladder and pancreatic tissue and to distinguish these samples from other samples on this panel. In addition, therapeutic modulation of the expression or function of this gene product may be useful in the

5   treatment of infection, inflammation and cancer of these tissues.

Panel 4.1D Summary: Ag4156 Expression of the CG97800-01 gene is limited to a few samples with highest expression in LAK cells treated with PMA/ionomycin (CT=33.5). Low, but significant expression is also seen in TNF-alpha and LPS treated neutrophils, untreated dendritic cells, LPS treated monocytes and IL-2 treated resting NK

10 cells. LAK cells are involved in tumor immunology and cell clearance of virally and bacterial infected cells as well as tumors. Therefore, modulation of the function of the protein encoded by this gene through the application of a small molecule drug or antibody may alter the functions of these cells and lead to improvement of symptoms associated with these conditions.

15 ### V. CG98092-01: Collagen like protein

Expression of gene CG98092-01 was assessed using the primer-probe sets Ag1964 and Ag4143, described in Tables VA and VB. Results of the RTQ-PCR runs are shown in Tables VC, VD, VE, VF, VG, VH and VI.

Table VA. Probe Name Ag1964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-caggggaggggtgagatag-3'	19	2595	
Probe	TET-5'-ctctgccatgccctccagctaggag-3'-TAMRA	25	2628	
Reverse	5'-tccaatcctctctgactcaaga-3'	22	2655	

20 Table VB. Probe Name Ag4143

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cccttaattggtgagatcttca-3'	22	1958	
Probe	TET-5'-ccgacctttcccttttgtccagtttt-3'-TAMRA	26	1990	
Reverse	5'-cttacactcggaaagcaaacaa-3'	22	2034	

Table VC. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag1964, Run 207634472	Rel. Exp.(%) Ag4143, Run 215294679	Tissue Name	Rel. Exp.(%) Ag1964, Run 207634472	Rel. Exp.(%) Ag4143, Run 215294679
AD 1 Hippo	8.1	6.1	Control (Path) 3 Temporal Ctx	3.2	5.4
AD 2 Hippo	10.4	8.6	Control (Path) 4 Temporal Ctx	34.6	54.7
AD 3 Hippo	4.8	7.7	AD 1 Occipital Ctx	6.1	8.9
AD 4 Hippo	4.5	12.3	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 Hippo	52.5	46.0	AD 3 Occipital Ctx	3.9	2.4
AD 6 Hippo	23.0	23.0	AD 4 Occipital Ctx	11.3	9.3
Control 2 Hippo	14.9	17.1	AD 5 Occipital Ctx	21.9	22.7
Control 4 Hippo	1.4	2.3	AD 6 Occipital Ctx	16.7	13.8
Control (Path) 3 Hippo	3.0	4.0	Control 1 Occipital Ctx	1.2	1.9
AD 1 Temporal Ctx	5.4	12.3	Control 2 Occipital Ctx	17.9	17.8
AD 2 Temporal Ctx	27.4	31.6	Control 3 Occipital Ctx	7.5	18.2
AD 3 Temporal Ctx	5.0	14.9	Control 4 Occipital Ctx	1.1	7.2
AD 4 Temporal	17.6	27.5	Control (Path) 1	83.5	90.8

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Ctx			Occipital Ctx		
AD 5 Inf Temporal Ctx	90.8	**100.0**	Control (Path) 2 Occipital Ctx	6.9	8.8
AD 5 Sup Temporal Ctx	19.9	24.7	Control (Path) 3 Occipital Ctx	2.8	1.6
AD 6 Inf Temporal Ctx	48.0	55.9	Control (Path) 4 Occipital Ctx	9.2	9.0
AD 6 Sup Temporal Ctx	39.2	51.8	Control 1 Parietal Ctx	5.1	7.7
Control 1 Temporal Ctx	6.1	6.3	Control 2 Parietal Ctx	45.7	62.4
Control 2 Temporal Ctx	46.7	34.4	Control 3 Parietal Ctx	10.7	20.3
Control 3 Temporal Ctx	18.3	17.9	Control (Path) 1 Parietal Ctx	84.7	66.0
Control 3 Temporal Ctx	11.1	7.0	Control (Path) 2 Parietal Ctx	21.3	20.6
Control (Path) 1 Temporal Ctx	**100.0**	88.3	Control (Path) 3 Parietal Ctx	6.1	4.4
Control (Path) 2 Temporal Ctx	52.5	57.0	Control (Path) 4 Parietal Ctx	38.4	41.8

Table VD. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4143, Run 221000251	Tissue Name	Rel. Exp.(%) Ag4143, Run 221000251
Adipose	1.4	Renal ca. TK-10	28.7
Melanoma* Hs688(A).T	1.9	Bladder	6.1
Melanoma* Hs688(B).T	2.7	Gastric ca. (liver met.) NCI-N87	40.3
Melanoma* M14	5.8	Gastric ca. KATO III	0.1
Melanoma* LOXIMVI	14.2	Colon ca. SW-948	9.3
Melanoma* SK-MEL-5	6.4	Colon ca. SW480	49.7
Squamous cell carcinoma SCC-4	8.3	Colon ca.* (SW480 met) SW620	33.9
Testis Pool	6.3	Colon ca. HT29	13.2
Prostate ca.* (bone met) PC-3	15.8	Colon ca. HCT-116	94.6
Prostate Pool	0.6	Colon ca. CaCo-2	21.5
Placenta	1.6	Colon cancer tissue	4.2
Uterus Pool	0.2	Colon ca. SW1116	12.6
Ovarian ca. OVCAR-3	14.0	Colon ca. Colo-205	3.0
Ovarian ca. SK-OV-3	19.2	Colon ca. SW-48	9.3
Ovarian ca. OVCAR-4	5.3	Colon Pool	1.4
Ovarian ca. OVCAR-5	27.5	Small Intestine Pool	0.7
Ovarian ca. IGROV-1	17.7	Stomach Pool	0.9
Ovarian ca. OVCAR-8	8.4	Bone Marrow Pool	0.3
Ovary	0.7	Fetal Heart	0.3
Breast ca. MCF-7	4.2	Heart Pool	0.2
Breast ca. MDA-MB-231	31.0	Lymph Node Pool	1.0
Breast ca. BT 549	20.4	Fetal Skeletal Muscle	0.4
Breast ca. T47D	59.5	Skeletal Muscle Pool	0.2
Breast ca. MDA-N	6.2	Spleen Pool	1.0
Breast Pool	1.2	Thymus Pool	1.8
Trachea	0.7	CNS cancer	5.8

		(glio/astro) U87-MG	
Lung	0.2	CNS cancer (glio/astro) U-118-MG	12.6
Fetal Lung	2.0	CNS cancer (neuro;met) SK-N-AS	34.9
Lung ca. NCI-N417	11.3	CNS cancer (astro) SF-539	2.3
Lung ca. LX-1	19.2	CNS cancer (astro) SNB-75	16.6
Lung ca. NCI-H146	7.0	CNS cancer (glio) SNB-19	13.9
Lung ca. SHP-77	29.1	CNS cancer (glio) SF-295	28.7
Lung ca. A549	24.3	Brain (Amygdala) Pool	6.5
Lung ca. NCI-H526	9.3	Brain (cerebellum)	5.5
Lung ca. NCI-H23	42.3	Brain (fetal)	2.8
Lung ca. NCI-H460	11.2	Brain (Hippocampus) Pool	4.2
Lung ca. HOP-62	9.8	Cerebral Cortex Pool	9.7
Lung ca. NCI-H522	**100.0**	Brain (Substantia nigra) Pool	9.6
Liver	0.5	Brain (Thalamus) Pool	15.2
Fetal Liver	0.7	Brain (whole)	18.2
Liver ca. HepG2	41.2	Spinal Cord Pool	1.3
Kidney Pool	0.7	Adrenal Gland	2.5
Fetal Kidney	0.9	Pituitary gland Pool	0.0
Renal ca. 786-0	0.2	Salivary Gland	1.1
Renal ca. A498	2.0	Thyroid (female)	0.5
Renal ca. ACHN	3.8	Pancreatic ca. CAPAN2	6.3
Renal ca. UO-31	0.7	Pancreas Pool	3.3

Table VE. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag1964, Run 149743240	Tissue Name	Rel. Exp.(%) Ag1964, Run 149743240
Liver adenocarcinoma	17.3	Kidney (fetal)	1.6
Pancreas	1.7	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	1.8	Renal ca. A498	9.8
Adrenal gland	6.7	Renal ca. RXF 393	1.7
Thyroid	1.5	Renal ca. ACHN	2.2
Salivary gland	1.4	Renal ca. UO-31	0.5
Pituitary gland	0.7	Renal ca. TK-10	3.4
Brain (fetal)	3.5	Liver	1.9
Brain (whole)	33.0	Liver (fetal)	2.9
Brain (amygdala)	26.4	Liver ca. (hepatoblast) HepG2	27.5
Brain (cerebellum)	2.0	Lung	1.7
Brain (hippocampus)	**100.0**	Lung (fetal)	3.3
Brain (substantia nigra)	1.9	Lung ca. (small cell) LX-1	7.0
Brain (thalamus)	6.6	Lung ca. (small cell) NCI-H69	42.3
Cerebral Cortex	54.0	Lung ca. (s.cell var.) SHP-77	12.2
Spinal cord	0.6	Lung ca. (large cell)NCI-H460	6.0
glio/astro U87-MG	2.8	Lung ca. (non-sm. cell) A549	5.3
glio/astro U-118-MG	7.0	Lung ca. (non-s.cell) NCI-H23	40.1
astrocytoma SW1783	12.6	Lung ca. (non-s.cell) HOP-62	7.1
neuro*; met SK-N-AS	29.1	Lung ca. (non-s.cl) NCI-H522	67.4
astrocytoma SF-539	1.2	Lung ca. (squam.) SW 900	1.6
astrocytoma SNB-75	4.6	Lung ca. (squam.) NCI-H596	10.5
glioma SNB-19	6.6	Mammary gland	5.5
glioma U251	2.9	Breast ca.* (pl.ef) MCF-7	3.4
glioma SF-295	13.7	Breast ca.* (pl.ef)	10.9

		MDA-MB-231	
Heart (fetal)	1.9	Breast ca.* (pl.ef) T47D	20.2
Heart	0.0	Breast ca. BT-549	10.6
Skeletal muscle (fetal)	11.8	Breast ca. MDA-N	3.7
Skeletal muscle	0.0	Ovary	4.2
Bone marrow	0.0	Ovarian ca. OVCAR-3	5.0
Thymus	1.1	Ovarian ca. OVCAR-4	1.1
Spleen	3.3	Ovarian ca. OVCAR-5	9.3
Lymph node	3.3	Ovarian ca. OVCAR-8	6.6
Colorectal	1.7	Ovarian ca. IGROV-1	4.4
Stomach	2.9	Ovarian ca.* (ascites) SK-OV-3	4.4
Small intestine	2.3	Uterus	1.8
Colon ca. SW480	32.5	Placenta	2.1
Colon ca.* SW620(SW480 met)	9.7	Prostate	5.5
Colon ca. HT29	5.4	Prostate ca.* (bone met)PC-3	8.7
Colon ca. HCT-116	18.6	Testis	44.4
Colon ca. CaCo-2	17.1	Melanoma Hs688(A).T	2.8
Colon ca. tissue(ODO3866)	5.2	Melanoma* (met) Hs688(B).T	3.5
Colon ca. HCC-2998	18.7	Melanoma UACC-62	4.7
Gastric ca.* (liver met) NCI-N87	21.8	Melanoma M14	2.7
Bladder	3.1	Melanoma LOX IMVI	5.3
Trachea	1.3	Melanoma* (met) SK-MEL-5	4.3
Kidney	0.7	Adipose	2.4

Table VF. Panel 2D

Tissue Name	Rel. Exp.(%) Ag1964, Run 162748484	Tissue Name	Rel. Exp.(%) Ag1964, Run 162748484
Normal Colon	6.2	Kidney Margin 8120608	5.6
CC Well to Mod Diff (ODO3866)	9.2	Kidney Cancer 8120613	1.5
CC Margin (ODO3866)	2.6	Kidney Margin 8120614	0.7
CC Gr.2 rectosigmoid (ODO3868)	6.8	Kidney Cancer 9010320	4.2
CC Margin (ODO3868)	0.8	Kidney Margin 9010321	3.8
CC Mod Diff (ODO3920)	18.0	Normal Uterus	4.6
CC Margin (ODO3920)	0.9	Uterus Cancer 064011	9.5
CC Gr.2 ascend colon (ODO3921)	84.1	Normal Thyroid	0.7
CC Margin (ODO3921)	1.5	Thyroid Cancer 064010	24.5
CC from Partial Hepatectomy (ODO4309) Mets	16.5	Thyroid Cancer A302152	10.6
Liver Margin (ODO4309)	19.5	Thyroid Margin A302153	2.9
Colon mets to lung (OD04451-01)	33.2	Normal Breast	26.1
Lung Margin (OD04451-02)	2.5	Breast Cancer (OD04566)	8.7
Normal Prostate 6546-1	48.6	Breast Cancer (OD04590-01)	12.3
Prostate Cancer (OD04410)	25.3	Breast Cancer Mets (OD04590-03)	14.9
Prostate Margin (OD04410)	5.0	Breast Cancer Metastasis (OD04655-05)	13.0
Prostate Cancer (OD04720-01)	3.2	Breast Cancer 064006	27.0
Prostate Margin (OD04720-02)	12.9	Breast Cancer 1024	50.0
Normal Lung 061010	11.0	Breast Cancer 9100266	15.7

Lung Met to Muscle (ODO4286)	23.8	Breast Margin 9100265	7.8
Muscle Margin (ODO4286)	3.0	Breast Cancer A209073	29.1
Lung Malignant Cancer (OD03126)	20.4	Breast Margin A209073	12.8
Lung Margin (OD03126)	5.5	Normal Liver	5.3
Lung Cancer (OD04404)	24.7	Liver Cancer 064003	2.7
Lung Margin (OD04404)	4.7	Liver Cancer 1025	7.8
Lung Cancer (OD04565)	34.2	Liver Cancer 1026	5.5
Lung Margin (OD04565)	4.0	Liver Cancer 6004-T	9.3
Lung Cancer (OD04237-01)	**100.0**	Liver Tissue 6004-N	11.1
Lung Margin (OD04237-02)	19.1	Liver Cancer 6005-T	6.8
Ocular Mel Met to Liver (ODO4310)	17.0	Liver Tissue 6005-N	5.7
Liver Margin (ODO4310)	9.6	Normal Bladder	17.3
Melanoma Mets to Lung (OD04321)	29.5	Bladder Cancer 1023	1.3
Lung Margin (OD04321)	5.6	Bladder Cancer A302173	9.8
Normal Kidney	4.0	Bladder Cancer (OD04718-01)	97.9
Kidney Ca, Nuclear grade 2 (OD04338)	10.5	Bladder Normal Adjacent (OD04718-03)	4.4
Kidney Margin (OD04338)	4.8	Normal Ovary	3.4
Kidney Ca Nuclear grade 1/2 (OD04339)	7.2	Ovarian Cancer 064008	21.9
Kidney Margin (OD04339)	1.8	Ovarian Cancer (OD04768-07)	2.8
Kidney Ca, Clear cell type (OD04340)	11.8	Ovary Margin (OD04768-08)	4.9
Kidney Margin (OD04340)	5.3	Normal Stomach	3.2
Kidney Ca, Nuclear	13.9	Gastric Cancer	2.4

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grade 3 (OD04348)		9060358	
Kidney Margin (OD04348)	2.1	Stomach Margin 9060359	6.2
Kidney Cancer (OD04622-01)	13.4	Gastric Cancer 9060395	7.3
Kidney Margin (OD04622-03)	0.1	Stomach Margin 9060394	7.5
Kidney Cancer (OD04450-01)	4.6	Gastric Cancer 9060397	18.3
Kidney Margin (OD04450-03)	1.8	Stomach Margin 9060396	1.6
Kidney Cancer 8120607	7.4	Gastric Cancer 064005	6.0

Table VG. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4143, Run 173119778	Tissue Name	Rel. Exp.(%) Ag4143, Run 173119778
Secondary Th1 act	43.2	HUVEC IL-1beta	2.1
Secondary Th2 act	37.4	HUVEC IFN gamma	2.4
Secondary Tr1 act	23.8	HUVEC TNF alpha + IFN gamma	2.5
Secondary Th1 rest	1.4	HUVEC TNF alpha + IL4	2.6
Secondary Th2 rest	1.3	HUVEC IL-11	1.0
Secondary Tr1 rest	0.7	Lung Microvascular EC none	2.1
Primary Th1 act	28.5	Lung Microvascular EC TNFalpha + IL-1beta	2.6
Primary Th2 act	45.1	Microvascular Dermal EC none	0.8
Primary Tr1 act	29.3	Microsvasular Dermal EC TNFalpha + IL-1beta	1.7
Primary Th1 rest	1.7	Bronchial epithelium TNFalpha + IL1beta	6.9
Primary Th2 rest	0.2	Small airway epithelium none	2.3
Primary Tr1 rest	1.3	Small airway epithelium TNFalpha + IL-1beta	4.6
CD45RA CD4 lymphocyte act	24.3	Coronery artery SMC rest	1.2
CD45RO CD4 lymphocyte act	34.9	Coronery artery SMC TNFalpha + IL-1beta	1.1
CD8 lymphocyte act	25.7	Astrocytes rest	1.6
Secondary CD8 lymphocyte rest	48.6	Astrocytes TNFalpha + IL-1beta	1.5
Secondary CD8 lymphocyte act	10.8	KU-812 (Basophil) rest	0.8
CD4 lymphocyte none	0.1	KU-812 (Basophil) PMA/ionomycin	0.7
2ry Th1/Th2/Tr1_anti-CD95 CH11	1.4	CCD1106 (Keratinocytes) none	6.2
LAK cells rest	13.5	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	5.4
LAK cells IL-2	11.0	Liver cirrhosis	1.2

LAK cells IL-2+IL-12	19.6	NCI-H292 none	4.3
LAK cells IL-2+IFN gamma	8.8	NCI-H292 IL-4	6.5
LAK cells IL-2+ IL-18	11.7	NCI-H292 IL-9	8.2
LAK cells PMA/ionomycin	**100.0**	NCI-H292 IL-13	4.7
NK Cells IL-2 rest	6.6	NCI-H292 IFN gamma	6.7
Two Way MLR 3 day	12.6	HPAEC none	0.7
Two Way MLR 5 day	29.9	HPAEC TNF alpha + IL-1 beta	4.3
Two Way MLR 7 day	19.9	Lung fibroblast none	0.5
PBMC rest	0.1	Lung fibroblast TNF alpha + IL-1 beta	1.4
PBMC PWM	30.6	Lung fibroblast IL-4	0.7
PBMC PHA-L	27.4	Lung fibroblast IL-9	0.6
Ramos (B cell) none	22.1	Lung fibroblast IL-13	1.0
Ramos (B cell) ionomycin	26.4	Lung fibroblast IFN gamma	0.6
B lymphocytes PWM	24.0	Dermal fibroblast CCD1070 rest	1.8
B lymphocytes CD40L and IL-4	6.1	Dermal fibroblast CCD1070 TNF alpha	2.0
EOL-1 dbcAMP	6.1	Dermal fibroblast CCD1070 IL-1 beta	1.9
EOL-1 dbcAMP PMA/ionomycin	1.9	Dermal fibroblast IFN gamma	0.6
Dendritic cells none	18.7	Dermal fibroblast IL-4	0.4
Dendritic cells LPS	70.7	Dermal Fibroblasts rest	0.3
Dendritic cells anti-CD40	16.8	Neutrophils TNFa+LPS	0.3
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	19.2	Colon	0.0
Macrophages rest	22.4	Lung	1.3
Macrophages LPS	47.0	Thymus	1.5
HUVEC none	1.6	Kidney	4.1
HUVEC starved	2.1		

Table VH. Panel 4D

Tissue Name	Rel. Exp.(%) Ag1964, Run 159038313	Tissue Name	Rel. Exp.(%) Ag1964, Run 159038313
Secondary Th1 act	46.3	HUVEC IL-1beta	0.7
Secondary Th2 act	29.1	HUVEC IFN gamma	1.7
Secondary Tr1 act	26.8	HUVEC TNF alpha + IFN gamma	1.5
Secondary Th1 rest	1.2	HUVEC TNF alpha + IL4	2.0
Secondary Th2 rest	1.5	HUVEC IL-11	0.9
Secondary Tr1 rest	0.9	Lung Microvascular EC none	0.8
Primary Th1 act	33.7	Lung Microvascular EC TNFalpha + IL-1beta	1.7
Primary Th2 act	27.5	Microvascular Dermal EC none	0.6
Primary Tr1 act	29.3	Microsvasular Dermal EC TNFalpha + IL-1beta	1.7
Primary Th1 rest	5.1	Bronchial epithelium TNFalpha + IL1beta	7.3
Primary Th2 rest	3.6	Small airway epithelium none	1.5
Primary Tr1 rest	0.7	Small airway epithelium TNFalpha + IL-1beta	7.4
CD45RA CD4 lymphocyte act	15.0	Coronery artery SMC rest	1.5
CD45RO CD4 lymphocyte act	27.5	Coronery artery SMC TNFalpha + IL-1beta	0.8
CD8 lymphocyte act	20.6	Astrocytes rest	1.4
Secondary CD8 lymphocyte rest	40.6	Astrocytes TNFalpha + IL-1beta	1.6
Secondary CD8 lymphocyte act	14.5	KU-812 (Basophil) rest	1.3
CD4 lymphocyte none	0.1	KU-812 (Basophil) PMA/ionomycin	0.7
2ry Th1/Th2/Tr1_anti-CD95 CH11	1.6	CCD1106 (Keratinocytes) none	3.6
LAK cells rest	10.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	2.4
LAK cells IL-2	11.0	Liver cirrhosis	0.9

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LAK cells IL-2+IL-12	14.9	Lupus kidney	0.1
LAK cells IL-2+IFN gamma	25.5	NCI-H292 none	4.6
LAK cells IL-2+ IL-18	26.2	NCI-H292 IL-4	8.1
LAK cells PMA/ionomycin	**100.0**	NCI-H292 IL-9	18.2
NK Cells IL-2 rest	6.2	NCI-H292 IL-13	6.7
Two Way MLR 3 day	12.8	NCI-H292 IFN gamma	7.9
Two Way MLR 5 day	34.9	HPAEC none	1.4
Two Way MLR 7 day	17.9	HPAEC TNF alpha + IL-1 beta	1.8
PBMC rest	0.2	Lung fibroblast none	0.3
PBMC PWM	57.8	Lung fibroblast TNF alpha + IL-1 beta	0.7
PBMC PHA-L	21.6	Lung fibroblast IL-4	0.8
Ramos (B cell) none	17.7	Lung fibroblast IL-9	0.2
Ramos (B cell) ionomycin	30.6	Lung fibroblast IL-13	0.4
B lymphocytes PWM	95.3	Lung fibroblast IFN gamma	0.4
B lymphocytes CD40L and IL-4	6.1	Dermal fibroblast CCD1070 rest	1.0
EOL-1 dbcAMP	3.9	Dermal fibroblast CCD1070 TNF alpha	6.0
EOL-1 dbcAMP PMA/ionomycin	1.6	Dermal fibroblast CCD1070 IL-1 beta	2.2
Dendritic cells none	17.1	Dermal fibroblast IFN gamma	0.8
Dendritic cells LPS	65.5	Dermal fibroblast IL-4	1.1
Dendritic cells anti-CD40	12.8	IBD Colitis 2	0.2
Monocytes rest	0.0	IBD Crohn's	0.3
Monocytes LPS	4.0	Colon	1.4
Macrophages rest	20.2	Lung	1.8
Macrophages LPS	59.9	Thymus	0.6
HUVEC none	1.7	Kidney	1.9
HUVEC starved	2.6		

Table VI. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4143, Run 268861689	Tissue Name	Rel. Exp.(%) Ag4143, Run 268861689
Colon cancer 1	0.0	Bladder cancer NAT 2	0.0
Colon cancer NAT 1	0.0	Bladder cancer NAT 3	0.0
Colon cancer 2	0.0	Bladder cancer NAT 4	0.0
Colon cancer NAT 2	0.0	Adenocarcinoma of the prostate 1	55.9
Colon cancer 3	0.2	Adenocarcinoma of the prostate 2	13.9
Colon cancer NAT 3	0.0	Adenocarcinoma of the prostate 3	0.2
Colon malignant cancer 4	0.1	Adenocarcinoma of the prostate 4	**100.0**
Colon normal adjacent tissue 4	0.1	Prostate cancer NAT 5	27.7
Lung cancer 1	0.1	Adenocarcinoma of the prostate 6	0.0
Lung NAT 1	0.0	Adenocarcinoma of the prostate 7	0.0
Lung cancer 2	0.1	Adenocarcinoma of the prostate 8	0.0
Lung NAT 2	0.0	Adenocarcinoma of the prostate 9	0.0
Squamous cell carcinoma 3	0.2	Prostate cancer NAT 10	52.9
Lung NAT 3	0.1	Kidney cancer 1	0.1
metastatic melanoma 1	0.0	KidneyNAT 1	0.1
Melanoma 2	0.0	Kidney cancer 2	0.3
Melanoma 3	0.0	Kidney NAT 2	0.1
metastatic melanoma 4	0.0	Kidney cancer 3	0.0
metastatic melanoma 5	0.0	Kidney NAT 3	0.0
Bladder cancer 1	0.0	Kidney cancer 4	0.0
Bladder cancer NAT 1	4.0	Kidney NAT 4	0.0
Bladder cancer 2	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag1964/Ag4143 Two experiments with two different probe and primer sets produce results that are in very good agreement.

Highest expression of the CG98092-01 gene is seen in the temporal cortex of an Alzheimer's patient in one experiment (CT=28.2) and in a control brain in the second (CT=30). Overall, this gene appears to be slightly down-regulated in the temporal cortex of Alzheimer's disease patients. Therefore, up-regulation of this gene or its protein

5   product, or treatment with specific agonists may be of use in reversing the dementia,memory loss and neuronal death associated with this disease.

General_screening_panel_v1.4 Summary: Ag4143 Highest expression of the CG98092-01 gene is seen in a lung cancer cell line (CT=26.4). This gene is widely expressed in the samples on this panel, with prominent expression in all the cancer cell

10   lines. Thus, expression of this gene could be used to differentiate between the lung cancer cell line and other samples on this panel and as a marker for lung cancer. Since cell lines are generally more proliferative than tissues, this gene might be involved in cell proliferation. Therefore, modulation of the expression or function of this gene may useful for the treatment of cancer or other disease that involve cell proliferation.

15   Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, fetal skeletal muscle and heart, and adult and fetal liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic function and that disregulated expression of this gene may contribute to neuroendocrine disorders

20   or metabolic diseases, such as obesity and diabetes.

In addition, this gene is expressed at much higher levels in fetal lung (CT=32) when compared to expression in the adult counterpart (CT=35). Thus, expression of this gene may be used to differentiate between the fetal and adult source of this tissue.

This gene is also expressed at moderate levels in the CNS, including the

25   hippocampus, thalamus, substantia nigra, amygdala, cerebellum and cerebral cortex. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Panel 1.3D Summary: Ag1964 Highest expression of the CG98092-01 gene is

30   seen in the hippocampus (CT=30.2). Moderate to low levels of expression are also seen in the amygdala, thalamus, and cortex. Please see Panel 1.4 for discussion of utility in the CNS.

Among metabolic tissues, low but significant levels of expression are seen in fetal skeletal muscle and the adrenal gland. Thus, this gene product may be involved in the pathogenesis and/or diagnosis of metabolic diseases that affect these tissues.

Moderate levels of expression are also seen in clusters of samples derived from
5   lung cancer, brain cancer, and colon cancer cell lines. Please see Panel 1.4 for further discussion of utility of this gene in cancer.

Panel 2D Summary: Ag1964 Highest expression of the CG98092-01 gene is seen in a lung cancer (CT=28). Significant levels of expression are also seen in lung, bladder, and colon cancers when compared to corresponding normal adjacent tissue. Thus,
10   expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of bladder, lung, and colon cancer.

Panel 4.1D Summary: Ag4143 Highest expression of the CG98092-01 gene is seen in LAK cells treated with PMA/ionomycin (CT=28.1). In addition, moderate levels of
15   expression are seen many hematopoietic cell types, including activated primary and secondary T cells, CD8 and CD4 lymphocytes, PWM treated PBMC and B lymphocytes, and activated dendritic cells, macrophages and monocytes. Thus, therapeutic modulation of the expression or function of this gene may reduce or eliminate symptoms in patients with autoimmune and inflammatory diseases such as, but not limited to, including Crohn's
20   disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, lupus erythematosus, or psoriasis.

Panel 4D Summary: Ag1964 Highest expression of the CG98092-01 gene is seen in LAK cells treated with PMA/ionomycin (CT=27.3). In addition, moderate levels of expression are seen many hematopoietic cell types, including activated primary and
25   secondary T cells, CD8 and CD4 lymphocytes, PWM treated PBMC and B lymphocytes, and activated dendritic cells, macrophages and monocytes. Thus, therapeutic modulation of the expression or function of this gene may reduce or eliminate symptoms in patients with autoimmune and inflammatory diseases such as, but not limited to, including Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease,
30   asthma, emphysema, rheumatoid arthritis, lupus erythematosus, or psoriasis.

General oncology screening panel_v_2.4 Summary: Ag4143 Expression of the CG98092-01 gene appears to be limited to prostate derived tissue, with highest expression in a prostate cancer sample (CT=28). Thus, expression of this gene could be used to

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differentiate between prostate derived tissue and other samples on this panel and as a marker of prostate tissue.

W. CG98121-01: MMTV-R-like cytokine

Expression of gene CG98121-01 was assessed using the primer-probe set Ag1984, described in Table WA. Results of the RTQ-PCR runs are shown in Tables WB, WC, WD and WE.

Table WA. Probe Name Ag1984

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctacaagccacctcacacaaa-3'	21	912	230
Probe	TET-5'-aggcctttcaccgagatcctcttgtt-3'-TAMRA	26	876	231
Reverse	5'-gctggggattcataatgagaat-3'	22	852	232

Table WB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag1984, Run 207794787	Tissue Name	Rel. Exp.(%) Ag1984, Run 207794787
AD 1 Hippo	19.8	Control (Path) 3 Temporal Ctx	4.4
AD 2 Hippo	17.6	Control (Path) 4 Temporal Ctx	18.7
AD 3 Hippo	6.7	AD 1 Occipital Ctx	5.4
AD 4 Hippo	6.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	32.1	AD 3 Occipital Ctx	6.8
AD 6 Hippo	**100.0**	AD 4 Occipital Ctx	12.5
Control 2 Hippo	12.2	AD 5 Occipital Ctx	11.3
Control 4 Hippo	14.4	AD 6 Occipital Ctx	24.1
Control (Path) 3 Hippo	12.2	Control 1 Occipital Ctx	3.0
AD 1 Temporal Ctx	11.7	Control 2 Occipital Ctx	17.3
AD 2 Temporal Ctx	11.0	Control 3 Occipital Ctx	7.3
AD 3 Temporal Ctx	5.6	Control 4 Occipital Ctx	4.8
AD 4 Temporal Ctx	11.2	Control (Path) 1 Occipital Ctx	21.3
AD 5 Inf Temporal Ctx	41.2	Control (Path) 2 Occipital Ctx	4.4
AD 5 Sup Temporal Ctx	43.8	Control (Path) 3 Occipital Ctx	9.6
AD 6 Inf Temporal Ctx	52.1	Control (Path) 4 Occipital Ctx	11.7
AD 6 Sup Temporal Ctx	49.3	Control 1 Parietal Ctx	4.8
Control 1 Temporal Ctx	5.3	Control 2 Parietal Ctx	20.9
Control 2 Temporal Ctx	15.7	Control 3 Parietal Ctx	5.0
Control 3 Temporal Ctx	4.1	Control (Path) 1 Parietal Ctx	14.8
Control 3	4.6	Control (Path) 2	5.3

Temporal Ctx		Parietal Ctx	
Control (Path) 1 Temporal Ctx	15.6	Control (Path) 3 Parietal Ctx	7.6
Control (Path) 2 Temporal Ctx	8.8	Control (Path) 4 Parietal Ctx	18.7

Table WC. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag1984, Run 147745098	Tissue Name	Rel. Exp.(%) Ag1984, Run 147745098
Liver adenocarcinoma	2.6	Kidney (fetal)	4.9
Pancreas	2.5	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	1.2	Renal ca. A498	12.9
Adrenal gland	15.9	Renal ca. RXF 393	0.6
Thyroid	2.1	Renal ca. ACHN	4.8
Salivary gland	2.0	Renal ca. UO-31	0.2
Pituitary gland	5.8	Renal ca. TK-10	3.3
Brain (fetal)	2.0	Liver	1.2
Brain (whole)	7.8	Liver (fetal)	7.5
Brain (amygdala)	4.9	Liver ca. (hepatoblast) HepG2	0.0
Brain (cerebellum)	2.1	Lung	26.8
Brain (hippocampus)	8.2	Lung (fetal)	16.2
Brain (substantia nigra)	6.5	Lung ca. (small cell) LX-1	4.3
Brain (thalamus)	11.4	Lung ca. (small cell) NCI-H69	0.2
Cerebral Cortex	16.5	Lung ca. (s.cell var.) SHP-77	14.3
Spinal cord	14.1	Lung ca. (large cell)NCI-H460	7.9
glio/astro U87-MG	3.3	Lung ca. (non-sm. cell) A549	5.6
glio/astro U-118-MG	0.3	Lung ca. (non-s.cell) NCI-H23	0.0
astrocytoma SW1783	0.3	Lung ca. (non-s.cell) HOP-62	1.0
neuro*; met SK-N-AS	**100.0**	Lung ca. (non-s.cl) NCI-H522	1.2
astrocytoma SF-539	6.0	Lung ca. (squam.) SW 900	7.2
astrocytoma SNB-75	18.7	Lung ca. (squam.) NCI-H596	0.0
glioma SNB-19	2.2	Mammary gland	21.8
glioma U251	0.5	Breast ca.* (pl.ef) MCF-7	0.0
glioma SF-295	0.9	Breast ca.* (pl.ef)	4.5

		MDA-MB-231	
Heart (fetal)	11.8	Breast ca.* (pl.ef) T47D	0.0
Heart	5.1	Breast ca. BT-549	4.6
Skeletal muscle (fetal)	22.8	Breast ca. MDA-N	27.5
Skeletal muscle	3.1	Ovary	8.1
Bone marrow	5.1	Ovarian ca. OVCAR-3	2.0
Thymus	2.4	Ovarian ca. OVCAR-4	0.0
Spleen	8.5	Ovarian ca. OVCAR-5	3.8
Lymph node	4.7	Ovarian ca. OVCAR-8	0.9
Colorectal	1.4	Ovarian ca. IGROV-1	1.1
Stomach	8.4	Ovarian ca.* (ascites) SK-OV-3	1.4
Small intestine	2.5	Uterus	5.1
Colon ca. SW480	12.1	Placenta	84.1
Colon ca.* SW620(SW480 met)	1.1	Prostate	1.7
Colon ca. HT29	6.5	Prostate ca.* (bone met)PC-3	2.1
Colon ca. HCT-116	8.3	Testis	5.4
Colon ca. CaCo-2	31.0	Melanoma Hs688(A).T	15.4
Colon ca. tissue(ODO3866)	13.6	Melanoma* (met) Hs688(B).T	11.3
Colon ca. HCC-2998	11.7	Melanoma UACC-62	4.6
Gastric ca.* (liver met) NCI-N87	20.7	Melanoma M14	9.2
Bladder	2.3	Melanoma LOX IMVI	0.6
Trachea	4.1	Melanoma* (met) SK-MEL-5	4.5
Kidney	2.2	Adipose	23.2

Table WD. Panel 2D

Tissue Name	Rel. Exp.(%) Ag1984, Run 147734781	Tissue Name	Rel. Exp.(%) Ag1984, Run 147734781
Normal Colon	38.2	Kidney Margin 8120608	17.3
CC Well to Mod Diff (ODO3866)	43.2	Kidney Cancer 8120613	6.5
CC Margin (ODO3866)	10.5	Kidney Margin 8120614	22.5
CC Gr.2 rectosigmoid (ODO3868)	9.1	Kidney Cancer 9010320	37.4
CC Margin (ODO3868)	6.0	Kidney Margin 9010321	33.7
CC Mod Diff (ODO3920)	26.2	Normal Uterus	5.4
CC Margin (ODO3920)	3.9	Uterus Cancer 064011	29.3
CC Gr.2 ascend colon (ODO3921)	45.4	Normal Thyroid	24.8
CC Margin (ODO3921)	3.7	Thyroid Cancer 064010	23.5
CC from Partial Hepatectomy (ODO4309) Mets	82.9	Thyroid Cancer A302152	11.1
Liver Margin (ODO4309)	23.2	Thyroid Margin A302153	17.8
Colon mets to lung (OD04451-01)	27.4	Normal Breast	44.8
Lung Margin (OD04451-02)	46.0	Breast Cancer (OD04566)	2.5
Normal Prostate 6546-1	21.5	Breast Cancer (OD04590-01)	12.4
Prostate Cancer (OD04410)	28.1	Breast Cancer Mets (OD04590-03)	42.6
Prostate Margin (OD04410)	22.4	Breast Cancer Metastasis (OD04655-05)	8.7
Prostate Cancer (OD04720-01)	17.1	Breast Cancer 064006	8.0
Prostate Margin (OD04720-02)	36.9	Breast Cancer 1024	9.4
Normal Lung 061010	91.4	Breast Cancer 9100266	8.2

Lung Met to Muscle (ODO4286)	32.3	Breast Margin 9100265	10.2
Muscle Margin (ODO4286)	14.4	Breast Cancer A209073	14.9
Lung Malignant Cancer (OD03126)	32.1	Breast Margin A209073	10.2
Lung Margin (OD03126)	**100.0**	Normal Liver	10.9
Lung Cancer (OD04404)	72.7	Liver Cancer 064003	15.1
Lung Margin (OD04404)	33.0	Liver Cancer 1025	8.8
Lung Cancer (OD04565)	43.2	Liver Cancer 1026	16.4
Lung Margin (OD04565)	25.5	Liver Cancer 6004-T	8.3
Lung Cancer (OD04237-01)	23.3	Liver Tissue 6004-N	29.5
Lung Margin (OD04237-02)	63.7	Liver Cancer 6005-T	12.6
Ocular Mel Met to Liver (ODO4310)	50.3	Liver Tissue 6005-N	4.7
Liver Margin (ODO4310)	10.4	Normal Bladder	44.1
Melanoma Mets to Lung (OD04321)	77.4	Bladder Cancer 1023	24.3
Lung Margin (OD04321)	68.8	Bladder Cancer A302173	4.6
Normal Kidney	63.7	Bladder Cancer (OD04718-01)	29.7
Kidney Ca, Nuclear grade 2 (OD04338)	26.2	Bladder Normal Adjacent (OD04718-03)	22.4
Kidney Margin (OD04338)	46.7	Normal Ovary	17.8
Kidney Ca Nuclear grade 1/2 (OD04339)	9.5	Ovarian Cancer 064008	39.2
Kidney Margin (OD04339)	45.1	Ovarian Cancer (OD04768-07)	8.8
Kidney Ca, Clear cell type (OD04340)	31.0	Ovary Margin (OD04768-08)	12.2
Kidney Margin (OD04340)	62.4	Normal Stomach	14.4
Kidney Ca, Nuclear	9.6	Gastric Cancer	7.0

grade 3 (OD04348)		9060358	
Kidney Margin (OD04348)	47.0	Stomach Margin 9060359	12.4
Kidney Cancer (OD04622-01)	8.4	Gastric Cancer 9060395	19.9
Kidney Margin (OD04622-03)	5.9	Stomach Margin 9060394	24.0
Kidney Cancer (OD04450-01)	11.0	Gastric Cancer 9060397	33.7
Kidney Margin (OD04450-03)	40.1	Stomach Margin 9060396	6.9
Kidney Cancer 8120607	17.1	Gastric Cancer 064005	19.8

Table WE. Panel 4D

Tissue Name	Rel. Exp.(%) Ag1984, Run 162350942	Tissue Name	Rel. Exp.(%) Ag1984, Run 162350942
Secondary Th1 act	9.5	HUVEC IL-1beta	1.1
Secondary Th2 act	8.0	HUVEC IFN gamma	3.3
Secondary Tr1 act	6.8	HUVEC TNF alpha + IFN gamma	1.1
Secondary Th1 rest	0.7	HUVEC TNF alpha + IL4	0.7
Secondary Th2 rest	1.1	HUVEC IL-11	1.2
Secondary Tr1 rest	1.1	Lung Microvascular EC none	3.5
Primary Th1 act	8.4	Lung Microvascular EC TNFalpha + IL-1beta	1.4
Primary Th2 act	5.2	Microvascular Dermal EC none	11.3
Primary Tr1 act	6.4	Microsvasular Dermal EC TNFalpha + IL-1beta	2.4
Primary Th1 rest	3.4	Bronchial epithelium TNFalpha + IL1beta	4.3
Primary Th2 rest	1.9	Small airway epithelium none	1.0
Primary Tr1 rest	1.6	Small airway epithelium TNFalpha + IL-1beta	4.5
CD45RA CD4 lymphocyte act	4.0	Coronery artery SMC rest	0.9
CD45RO CD4 lymphocyte act	7.5	Coronery artery SMC TNFalpha + IL-1beta	0.5
CD8 lymphocyte act	4.2	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	6.4	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	3.3	KU-812 (Basophil) rest	55.9
CD4 lymphocyte none	0.6	KU-812 (Basophil) PMA/ionomycin	**100.0**
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.6	CCD1106 (Keratinocytes) none	1.4
LAK cells rest	2.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.8
LAK cells IL-2	5.1	Liver cirrhosis	1.0

LAK cells IL-2+IL-12	7.8	Lupus kidney	0.8
LAK cells IL-2+IFN gamma	6.4	NCI-H292 none	4.5
LAK cells IL-2+ IL-18	3.9	NCI-H292 IL-4	5.0
LAK cells PMA/ionomycin	3.7	NCI-H292 IL-9	5.8
NK Cells IL-2 rest	3.1	NCI-H292 IL-13	3.9
Two Way MLR 3 day	3.1	NCI-H292 IFN gamma	5.6
Two Way MLR 5 day	4.0	HPAEC none	3.1
Two Way MLR 7 day	3.9	HPAEC TNF alpha + IL-1 beta	1.3
PBMC rest	0.7	Lung fibroblast none	1.0
PBMC PWM	17.3	Lung fibroblast TNF alpha + IL-1 beta	1.0
PBMC PHA-L	6.4	Lung fibroblast IL-4	5.6
Ramos (B cell) none	4.0	Lung fibroblast IL-9	3.8
Ramos (B cell) ionomycin	10.7	Lung fibroblast IL-13	3.4
B lymphocytes PWM	21.9	Lung fibroblast IFN gamma	8.6
B lymphocytes CD40L and IL-4	3.0	Dermal fibroblast CCD1070 rest	3.2
EOL-1 dbcAMP	3.7	Dermal fibroblast CCD1070 TNF alpha	5.8
EOL-1 dbcAMP PMA/ionomycin	1.8	Dermal fibroblast CCD1070 IL-1 beta	2.3
Dendritic cells none	2.3	Dermal fibroblast IFN gamma	1.4
Dendritic cells LPS	2.4	Dermal fibroblast IL-4	1.7
Dendritic cells anti-CD40	3.6	IBD Colitis 2	0.1
Monocytes rest	1.0	IBD Crohn's	0.1
Monocytes LPS	2.3	Colon	1.0
Macrophages rest	1.9	Lung	15.8
Macrophages LPS	1.1	Thymus	4.3
HUVEC none	2.1	Kidney	2.2
HUVEC starved	13.4		

CNS_neurodegeneration_v1.0 Summary: Ag1984 This panel confirms the expression of the CG98121-01 gene at moderate levels in the brain in an independent group of individuals. This gene is found to be upregulated in the temporal cortex of

Alzheimer's disease patients. Therefore, therapeutic inhibition of this protein may be of use in the treatment of this disease and decrease neuronal death.

Panel 1.3D Summary: Ag1984 Highest expression of the CG98121-01 gene is seen in a neuroblastoma cell line(CT=29.7). Thus, expression of this gene could be used to

5   differentiate between this sample and other samples and as a marker for this cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of brain cancer.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, fetal liver, and adult and fetal skeletal muscle

10   and heart. This expression suggests that this gene product may play a role in normal neuroendocrine and metabolic function and that disregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This gene is also expressed at low levels in the CNS, including the hippocampus, thalamus, substantia nigra, amygdala, and cerebral cortex. Therefore, therapeutic

15   modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Panel 2D Summary: Ag1984 Highest expression of the CG98121-01 gene is seen in normal lung (CT=31.1). Significant expression is also seen in colon cancer when

20   compared to normal adjacent tissue and conversely in kidney when compared to adjacent tumor. Thus, therapeutic modulation of the expression or function of this protein may be useful in the treatment of kidney and colon cancer.

Panel 4D Summary: Ag1984 The CG98121-01 transcript is induced in the PMA and ionomycin treated basophil cell line KU-812 (CT=27.5). Basophils release histamines

25   and other biological modifiers in reponse to allergens and play an important role in the pathology of asthma and hypersensitivity reactions. Therefore, therapeutics designed against the putative protein encoded by this gene may reduce or inhibit inflammation by blocking basophil function in these diseases. In addition, these cells are a reasonable model for the inflammatory cells that take part in various inflammatory lung and bowel

30   diseases, such as asthma, Crohn's disease, and ulcers.

Example D: Identification of Single Nucleotide Polymorphisms in NOVX nucleic acid sequences

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Variant sequences are also included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due

5   to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the

10   amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, when a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern. Examples include alteration in

15   temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, and stability of transcribed message.

SeqCalling assemblies produced by the exon linking process were selected and extended using the following criteria. Genomic clones having regions with 98% identity to all or part of the initial or extended sequence were identified by BLASTN searches

20   using the relevant sequence to query human genomic databases. The genomic clones that resulted were selected for further analysis because this identity indicates that these clones contain the genomic locus for these SeqCalling assemblies. These sequences were analyzed for putative coding regions as well as for similarity to the known DNA and protein sequences. Programs used for these analyses include Grail, Genscan, BLAST,

25   HMMER, FASTA, Hybrid and other relevant programs.

Some additional genomic regions may have also been identified because selected SeqCalling assemblies map to those regions. Such SeqCalling sequences may have overlapped with regions defined by homology or exon prediction. They may also be included because the location of the fragment was in the vicinity of genomic regions

30   identified by similarity or exon prediction that had been included in the original predicted sequence. The sequence so identified was manually assembled and then may have been extended using one or more additional sequences taken from CuraGen Corporation's human SeqCalling database. SeqCalling fragments suitable for inclusion were identified

by the CuraTools™ program SeqExtend or by identifying SeqCalling fragments mapping to the appropriate regions of the genomic clones analyzed.

The regions defined by the procedures described above were then manually integrated and corrected for apparent inconsistencies that may have arisen, for example,

5   from miscalled bases in the original fragments or from discrepancies between predicted exon junctions, EST locations and regions of sequence similarity, to derive the final sequence disclosed herein. When necessary, the process to identify and analyze SeqCalling assemblies and genomic clones was reiterated to derive the full length sequence (Alderborn et al., Determination of Single Nucleotide Polymorphisms by

10   Real-time Pyrophosphate DNA Sequencing. Genome Research. 10 (8) 1249-1265, 2000).

Variants are reported individually but any combination of all or a select subset of variants are also included as contemplated NOVX embodiments of the invention.

Table 1. Variants of NOV2a (CG105716-01).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378855	1304	A	G	435	Asp	Gly
13378856	1434	T	C	478	Pro	Pro

15   Table 2. Variants of NOV5a (CG57415-01).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378905	508	G	A	151	Gly	Glu
13378904	571	T	C	172	Val	Ala
13378903	606	G	A	184	Val	Ile
13378902	1506	G	T	484	Gly	End
13378901	2324	T	C	756	Asp	Asp
13378900	2812	T	C	919	Leu	Pro

Table 3. Variants of NOV7b (CG58586-02).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378884	3614	C	T	1199	Thr	Thr
13378883	4000	G	A	0		
13378882	4106	G	A	0		

Table 4. Variants of NOV8a (CG93453-01).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378906	501	G	A	138	Arg	Lys
13378907	3455	A	G	1123	Lys	Glu
13378878	3476	C	T	1130	Arg	Cys

5   Table 5. Variants of NOV9a (CG95145-01).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378893	387	C	A	113	Arg	Arg
13378892	427	C	T	126	Ala	Val
13378889	641	C	T	197	Cys	Cys
13374671	647	A	G	199	Val	Val

Table 6. Variant of NOV12a (CG95794-01).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378958	763	A	G	252	Asn	Ser

10

Table 7. Variants of NOV14a (CG95861-01).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378962	504	G	T	153	Ala	Ser
13378985	605	A	G	186	Lys	Lys
13378961	698	C	G	217	Leu	Leu

Table 8. Variants of NOV15a (CG96412-01).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13375654	338	T	C	58	Leu	Pro
13375431	412	A	G	83	Arg	Gly
13375432	491	T	C	109	Val	Ala
13378984	505	C	G	114	Arg	Gly
13378983	534	T	C	123	Ser	Ser
13375433	536	T	C	124	Leu	Pro
13375434	547	T	C	128	Phe	Leu
13375435	593	T	C	143	Val	Ala
13375436	595	T	C	144	Ser	Pro
13375442	599	T	C	145	Phe	Ser
13375441	640	G	A	159	Val	Met
13375440	659	A	G	165	Lys	Arg
13375439	667	T	C	168	Ser	Pro
13375438	710	A	G	182	Lys	Arg
13378982	1100	A	G	312	His	Arg
13377875	1118	G	A	318	Arg	Gln
13377874	1180	C	G	339	Leu	Val
13378981	1188	T	C	341	Pro	Pro
13375444	1226	T	C	354	Leu	Pro
13375445	1297	A	G	378	Arg	Gly
13375545	1914	G	C	583	Val	Val
13378980	1951	C	T	596	Leu	Phe

5   Table 9. Variant of NOV19a (CG96567-02).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13374664	229	C	T	60	Ser	Leu

Table 10. Variants of NOV21a (CG97274-01).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378964	180	A	G	60	Ser	Gly
13376794	324	C	A	108	Leu	Met
13376795	355	A	G	118	Gln	Arg
13376796	375	G	A	125	Ala	Thr
13378965	410	G	A	136	Leu	Leu
13376797	417	T	C	139	Ser	Pro

Table 11. Variant of NOV24a (CG97550-01).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378959	802	C	T	203	Gln	End

5

Table 12. Variants of NOV26a (CG97800-01).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378957	197	G	T	48	Gln	His
13378956	274	A	G	74	His	Arg
13378960	304	T	C	84	Val	Ala
13378955	457	A	G	135	Asp	Gly
13378954	535	G	A	161	Gly	Asp
13378952	643	C	A	197	Pro	Gln
13378951	683	T	A	210	His	Gln

Table 13: Variants of NOV29a (CG99662-01).

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378976	265	T	C	83	Met	Thr
13378975	324	G	A	103	Gly	Arg
13378974	429	T	C	138	Ser	Pro
13378973	432	C	T	139	Arg	Cys
13378972	443	C	T	142	Gly	Gly
13378971	594	T	C	193	Phe	Leu
13378970	684	T	C	223	Ser	Pro
13378969	828	T	G	271	Trp	Gly
13378968	854	C	T	279	Gly	Gly

OTHER EMBODIMENTS

5

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims, which follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications

10   may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. The choice of nucleic acid starting material, clone of interest, or library type is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein. Other aspects, advantages, and modifications considered to be within the scope of the following claims. The claims

15   presented are representative of the inventions disclosed herein. Other, unclaimed inventions are also contemplated. Applicants reserve the right to pursue such inventions in later claims.

20

We claim:

What is claimed is:

5   1.   An isolated polypeptide comprising the mature form of an amino acid sequenced selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 62

2.   An isolated polypeptide comprising an amino acid sequence selected from the
10   group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 62.

3.   An isolated polypeptide comprising an amino acid sequence which is at least 95% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 62.

15

4.   An isolated polypeptide, wherein the polypeptide comprises an amino acid sequence comprising one or more conservative substitutions in the amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 62.

20

5.   The polypeptide of claim 1 wherein said polypeptide is naturally occurring.

6.   A composition comprising the polypeptide of claim 1 and a carrier.

25   7.   A kit comprising, in one or more containers, the composition of claim 6.

8.   The use of a therapeutic in the manufacture of a medicament for treating a syndrome associated with a human disease, the disease selected from a pathology associated with the polypeptide of claim 1, wherein the therapeutic comprises the
30   polypeptide of claim 1.

9.   A method for determining the presence or amount of the polypeptide of claim 1 in a sample, the method comprising:

        (a)   providing said sample;

(b)   introducing said sample to an antibody that binds immunospecifically to the polypeptide; and

(c)   determining the presence or amount of antibody bound to said polypeptide, thereby determining the presence or amount of polypeptide in said sample.

5

10.   A method for determining the presence of or predisposition to a disease associated with altered levels of expression of the polypeptide of claim 1 in a first mammalian subject, the method comprising:

a)   measuring the level of expression of the polypeptide in a sample from the first mammalian subject; and

10

b)   comparing the expression of said polypeptide in the sample of step (a) to the expression of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, said disease,

15   wherein an alteration in the level of expression of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to said disease.

11.   A method of identifying an agent that binds to the polypeptide of claim 1, the method comprising:

20

(a)   introducing said polypeptide to said agent; and

(b)   determining whether said agent binds to said polypeptide.

12.   The method of claim 11 wherein the agent is a cellular receptor or a downstream effector.

25

13.   A method for identifying a potential therapeutic agent for use in treatment of a pathology, wherein the pathology is related to aberrant expression or aberrant physiological interactions of the polypeptide of claim 1, the method comprising:

(a)   providing a cell expressing the polypeptide of claim 1 and having a property or function ascribable to the polypeptide;

30

(b)   contacting the cell with a composition comprising a candidate substance; and

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(c)   determining whether the substance alters the property or function ascribable
        to the polypeptide;

whereby, if an alteration observed in the presence of the substance is not observed when

the cell is contacted with a composition in the absence of the substance, the substance is

5   identified as a potential therapeutic agent.

14.   A method for screening for a modulator of activity of or of latency or
        predisposition to a pathology associated with the polypeptide of claim 1, said
        method comprising:

10   (a)   administering a test compound to a test animal at increased risk for a
                pathology associated with the polypeptide of claim 1, wherein said test
                animal recombinantly expresses the polypeptide of claim 1;

        (b)   measuring the activity of said polypeptide in said test animal after
                administering the compound of step (a); and

15   (c)   comparing the activity of said polypeptide in said test animal with the
                activity of said polypeptide in a control animal not administered said
                polypeptide, wherein a change in the activity of said polypeptide in said test
                animal relative to said control animal indicates the test compound is a
                modulator activity of or latency or predisposition to, a pathology associated

20   with the polypeptide of claim 1.

15.   The method of claim 14, wherein said test animal is a recombinant test animal that
        expresses a test protein transgene or expresses said transgene under the control of a
        promoter at an increased level relative to a wild-type test animal, and wherein said

25   promoter is not the native gene promoter of said transgene.

16.   A method for modulating the activity of the polypeptide of claim 1, the method
        comprising contacting a cell sample expressing the polypeptide of claim 1 with a
        compound that binds to said polypeptide in an amount sufficient to modulate the

30   activity of the polypeptide.

17.   A method of treating or preventing a pathology associated with the polypeptide of
        claim 1, the method comprising administering the polypeptide of claim 1 to a

subject in which such treatment or prevention is desired in an amount sufficient to treat or prevent the pathology in the subject.

18.   The method of claim 17, wherein the subject is a human.

5

19.   A method of treating a pathological state in a mammal, the method comprising administering to the mammal a polypeptide in an amount that is sufficient to alleviate the pathological state, wherein the polypeptide is a polypeptide having an amino acid sequence at least 95% identical to a polypeptide comprising the amino

10   acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 62 or a biologically active fragment thereof.

20.   An isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1

15   and 62.

21.   The nucleic acid molecule of claim 20, wherein the nucleic acid molecule is naturally occurring.

20   22.   A nucleic acid molecule, wherein the nucleic acid molecule differs by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 62.

...

23.   An isolated nucleic acid molecule encoding the mature form of a polypeptide

25   having an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 62.

24.   An isolated nucleic acid molecule comprising a nucleic acid selected from the group consisting of 2n-1, wherein n is an integer between 1 and 62.

30

25.   The nucleic acid molecule of claim 20, wherein said nucleic acid molecule hybridizes under stringent conditions to the nucleotide sequence selected from the

group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 62, or a complement of said nucleotide sequence.

5

26.   A vector comprising the nucleic acid molecule of claim 20.

27.   The vector of claim 26, further comprising a promoter operably linked to said nucleic acid molecule.

28.   A cell comprising the vector of claim 26.

10

29.   An antibody that immunospecifically binds to the polypeptide of claim 1.

30.   The antibody of claim 29, wherein the antibody is a monoclonal antibody.

15   31.   The antibody of claim 29, wherein the antibody is a humanized antibody.

32.   A method for determining the presence or amount of the nucleic acid molecule of claim 20 in a sample, the method comprising:

(a)   providing said sample;

20   (b)   introducing said sample to a probe that binds to said nucleic acid molecule; and

(c)   determining the presence or amount of said probe bound to said nucleic acid molecule,

thereby determining the presence or amount of the nucleic acid molecule in said sample.

25

33.   The method of claim 32 wherein presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type.

34.   The method of claim 33 wherein the cell or tissue type is cancerous.

30

35.   A method for determining the presence of or predisposition to a disease associated with altered levels of expression of the nucleic acid molecule of claim 20 in a first mammalian subject, the method comprising:

a) measuring the level of expression of the nucleic acid in a sample from the first mammalian subject; and

b) comparing the level of expression of said nucleic acid in the sample of step (a) to the level of expression of the nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease;

wherein an alteration in the level of expression of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.

36. A method of producing the polypeptide of claim 1, the method comprising culturing a cell under conditions that lead to expression of the polypeptide, wherein said cell comprises a vector comprising an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 62.

37. The method of claim 36 wherein the cell is a bacterial cell.

38. The method of claim 36 wherein the cell is an insect cell.

39. The method of claim 36 wherein the cell is a yeast cell.

40. The method of claim 36 wherein the cell is a mammalian cell.

41. A method of producing the polypeptide of claim 2, the method comprising culturing a cell under conditions that lead to expression of the polypeptide, wherein said cell comprises a vector comprising an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 62.

42. The method of claim 41 wherein the cell is a bacterial cell.

43. The method of claim 41 wherein the cell is an insect cell.

44.   The method of claim 41 wherein the cell is a yeast cell.

45.   The method of claim 41 wherein the cell is a mammalian cell.